GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 19:18:54 ; Search time 3648 Seconds
(without alignments)
12292.993 Million cell updates/sec

Title: US-10-798-896-1
Perfect score: 5423
Sequence: 1 ccaccgcggtggcggccgtc.....ctatagggcgaattggagct 5423

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5423	100.0	5423	9	US-10-798-896-1	Sequence 1, Appli
2	2237	41.3	2237	9	US-10-798-896-5	Sequence 5, Appli
3	2218	40.9	3599	3	US-09-861-101-3	Sequence 3, Appli
4	2218	40.9	3803	9	US-10-798-896-2	Sequence 2, Appli
5	2215.8	40.9	3600	3	US-09-861-101-2	Sequence 2, Appli
6	2211.6	40.8	3558	7	US-10-281-067B-26	Sequence 26, Appl
7	2211.6	40.8	3558	8	US-10-764-818A-26	Sequence 26, Appl
8	2160	39.8	2192	5	US-10-021-403A-10	Sequence 10, Appl
9	2160	39.8	3534	5	US-10-021-403A-9	Sequence 9, Appli
10	2160	39.8	3534	7	US-10-395-709-11	Sequence 11, Appl
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42	2160	39.8	3534	8	US-10-764-818A-15	Sequence 15, Appl
43	2160	39.8	3534	8	US-10-764-818A-29	Sequence 29, Appl
44	2160	39.8	3534	8	US-10-827-918-11	Sequence 11, Appl
45	2160	39.8	3534	8	US-10-827-918-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-798-896-1
; Sequence 1, Application US/10798896
; Publication No. US20050238624A1
; GENERAL INFORMATION:
; APPLICANT: ADViSYS, Inc.
; TITLE OF INVENTION: Insulin-Like Growth Factor ("IGF-I") Plasmid Mediated Supplementa
; TITLE OF INVENTION: Therapeutic Applications
; FILE REFERENCE: 108328.00172 - AVSI-0034
; CURRENT APPLICATION NUMBER: US/10/798,896
; CURRENT FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5423
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acid sequence for the pAV2001 plasmid.
US-10-798-896-1

Query Match 100.0%; Score 5423; DB 9; Length 5423;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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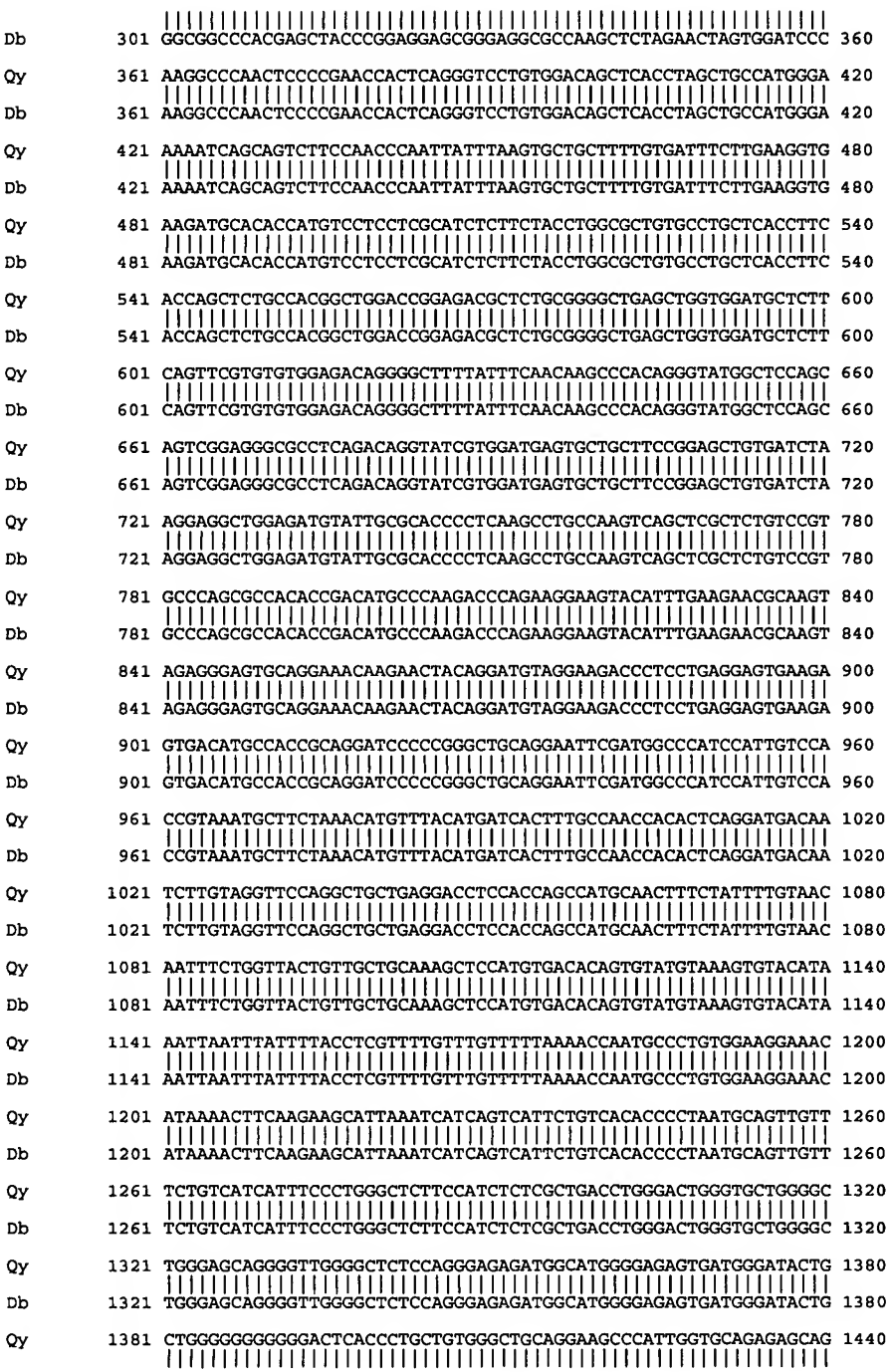
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Db      3961 TATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT 4020

Qy      4021 AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT 4080

Qy      4081 AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC 4140

Qy      4141 TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGT 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGT 4200

Qy      4201 TTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 TTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG 4260

Qy      4261 ATCTTTTCTACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 ATCTTTTCTACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATG 4320

Qy      4321 CGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCG 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 CGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCG 4380

Qy      4381 CCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACA 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 CCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACA 4440

Qy      4441 CCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGC 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 CCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGC 4500

Qy      4501 AAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGC 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 AAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGC 4560

Qy      4561 CTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 CTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCG 4620

Qy      4621 ACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCG 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 ACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCG 4680

Qy      4681 AATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGAT 4740
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 AATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGAT 4740

Qy       4741 ACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAAT 4800
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 ACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAAT 4800

Qy       4801 AGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCC 4860
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 AGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCC 4860

Qy       4861 GTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGAC 4920
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGAC 4920

Qy       4921 AGGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCA 4980
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 AGGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCA 4980

Qy       4981 TCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCG 5040
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 TCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCG 5040

Qy       5041 GCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTC 5100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 GCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTC 5100

Qy       5101 TCTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAG 5160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 TCTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAG 5160

Qy       5161 TTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCG 5220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 TTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCG 5220

Qy       5221 CTTGCTGTCCATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCC 5280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 CTTGCTGTCCATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCC 5280

Qy       5281 TCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTA 5340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5281 TCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTA 5340

Qy       5341 ACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGAC 5400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 ACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGAC 5400

Qy       5401 TCACTATAGGGCGAATTGGAGCT 5423
                |||||||||||||||||||||||
Db       5401 TCACTATAGGGCGAATTGGAGCT 5423


RESULT 2
US-10-798-896-5
; Sequence 5, Application US/10798896
; Publication No. US20050238624A1
; GENERAL INFORMATION:
;  APPLICANT: ADViSYS, Inc.
;  TITLE OF INVENTION: Insulin-Like Growth Factor ("IGF-I") Plasmid Mediated Supplementa
;  TITLE OF INVENTION:  Therapeutic Applications
;  FILE REFERENCE: 108328.00172 - AVSI-0034
;  CURRENT APPLICATION NUMBER: US/10/798,896
;  CURRENT FILING DATE:  2004-03-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 2237
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence for the skeletal alpha actin 3' end.
US-10-798-896-5
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  Query Match             41.3%;  Score 2237;  DB 9;  Length 2237;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2237;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        934 GGAATTCGATGGCCCATCCATTGTCCACCGTAAATGCTTCTAAACATGTTTACATGATCA 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAATTCGATGGCCCATCCATTGTCCACCGTAAATGCTTCTAAACATGTTTACATGATCA 60

Qy        994 CTTTGCCAACCACACTCAGGATGACAATCTTGTAGGTTCCAGGCTGCTGAGGACCTCCAC 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTTTGCCAACCACACTCAGGATGACAATCTTGTAGGTTCCAGGCTGCTGAGGACCTCCAC 120

Qy       1054 CAGCCATGCAACTTTCTATTTTGTAACAATTTCTGGTTACTGTTGCTGCAAAGCTCCATG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGCCATGCAACTTTCTATTTTGTAACAATTTCTGGTTACTGTTGCTGCAAAGCTCCATG 180

Qy       1114 TGACACAGTGTATGTAAAGTGTACATAAATTAATTTATTTTACCTCGTTTTGTTTGTTTT 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGACACAGTGTATGTAAAGTGTACATAAATTAATTTATTTTACCTCGTTTTGTTTGTTTT 240

Qy       1174 TAAAACCAATGCCCTGTGGAAGGAAACATAAAACTTCAAGAAGCATTAAATCATCAGTCA 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TAAAACCAATGCCCTGTGGAAGGAAACATAAAACTTCAAGAAGCATTAAATCATCAGTCA 300

Qy       1234 TTCTGTCACACCCCTAATGCAGTTGTTTCTGTCATCATTTCCCTGGGCTCTTCCATCTCT 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCTGTCACACCCCTAATGCAGTTGTTTCTGTCATCATTTCCCTGGGCTCTTCCATCTCT 360

Qy       1294 CGCTGACCTGGGACTGGGTGCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGA 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCTGACCTGGGACTGGGTGCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGA 420

Qy       1354 TGGCATGGGGAGAGTGATGGGATACTGCTGGGGGGGGGGGGACTCACCCTGCTGTGGGCTG 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGCATGGGGAGAGTGATGGGATACTGCTGGGGGGGGGGGGACTCACCCTGCTGTGGGCTG 480

Qy       1414 CAGGAAGCCCATTGGTGCAGAGAGCAGCCTGGGATGCCCATGACACGGGCACCCACTGCA 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGGAAGCCCATTGGTGCAGAGAGCAGCCTGGGATGCCCATGACACGGGCACCCACTGCA 540

Qy       1474 CCGTGTTTCTCCCATGCCCAGTAGGGAAAGGGTTACGAGCGCCGTTCATTCTCAGCTTGT 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCGTGTTTCTCCCATGCCCAGTAGGGAAAGGGTTACGAGCGCCGTTCATTCTCAGCTTGT 600

Qy       1534 GAAGGATTTTGTTGGGCTCAGCCTGCCAGAGCAGTAGCCAGGCATGCCTGTGCAGCTCCG 1593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAAGGATTTTGTTGGGCTCAGCCTGCCAGAGCAGTAGCCAGGCATGCCTGTGCAGCTCCG 660

Qy       1594 AGCTGTGATGGACAGAGGCAAGGCTGCAGCTGAGGCCAGGTGGTGGGCACAGGTTAAATT 1653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCTGTGATGGACAGAGGCAAGGCTGCAGCTGAGGCCAGGTGGTGGGCACAGGTTAAATT 720

Qy       1654 AAGAGCTTTCCACTCCACTTATGGAAAGCCCTCCTGCACTCACCCTGTCCCTGGGGCTGG 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGAGCTTTCCACTCCACTTATGGAAAGCCCTCCTGCACTCACCCTGTCCCTGGGGCTGG 780

Qy       1714 GGGCAGCCAGGGCCACTTCCTCACCCCACCTGACACACAAGGCTTTGCCTGCACAGCCAG 1773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGGCAGCCAGGGCCACTTCCTCACCCCACCTGACACACAAGGCTTTGCCTGCACAGCCAG 840

Qy       1774 GACCTCCTGTGGCCACAGACTCTTATAGATTCGCTGTGCCCTAGGAGACCAGGGGGCTTT 1833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCTCCTGTGGCCACAGACTCTTATAGATTCGCTGTGCCCTAGGAGACCAGGGGGCTTT 900

Qy       1834 CCCTGCCTGGCCTTCTGGCCCCGGCGACACTGCAGGAGCTGCCCTATCTGCCTCCTCTTA 1893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCCTGCCTGGCCTTCTGGCCCCGGCGACACTGCAGGAGCTGCCCTATCTGCCTCCTCTTA 960

Qy       1894 GATGGTCCTGGCAGGAAGGCTGCACTTGGCTTGGGGCTGATCCATATTACCACTGCAGTA 1953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GATGGTCCTGGCAGGAAGGCTGCACTTGGCTTGGGGCTGATCCATATTACCACTGCAGTA 1020

Qy       1954 GGGACAGCACTGCTGGAAGAAAAGATGATTTTCAACTGAACTTACTATCCAGGCAGGTTA 2013
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Db       1021 GGGACAGCACTGCTGGAAGAAAAGATGATTTTCAACTGAACTTACTATCCAGGCAGGTTA 1080

Qy       2014 TTGCTTTATTGTGATGGTGCTAAGAGTGCGTTCTTTCTCACTGTAATGATTTTGCCCTCA 2073
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTGCTTTATTGTGATGGTGCTAAGAGTGCGTTCTTTCTCACTGTAATGATTTTGCCCTCA 1140

Qy       2074 TGTGTGAATACACTTTCCAATAACAGCACAGCCTCCAAAGGGAATTTCTGCAGGAAGAGA 2133
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TGTGTGAATACACTTTCCAATAACAGCACAGCCTCCAAAGGGAATTTCTGCAGGAAGAGA 1200

Qy       2134 CAGTACCTGGTGTGGGAAGTCCCTGTGCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGA 2193
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGTACCTGGTGTGGGAAGTCCCTGTGCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGA 1260

Qy       2194 CTGGCTGGGAGAGCAGGATCACATCCTTTCTTAAAAAGACAAACAGAAGGTAGTGTGTGA 2253
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTGGCTGGGAGAGCAGGATCACATCCTTTCTTAAAAAGACAAACAGAAGGTAGTGTGTGA 1320

Qy       2254 CCTTGCTGTATTTACTATTTACGCGTTGTTGTTCAGTGGCACATACCTCAACGGGGATAT 2313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTTGCTGTATTTACTATTTACGCGTTGTTGTTCAGTGGCACATACCTCAACGGGGATAT 1380

Qy       2314 GGAGAGCTATTTCCCCAACCCTCGCTGCTGGACCCTGATCTGGGGTTTTCCTGTAGCTTA 2373
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGAGAGCTATTTCCCCAACCCTCGCTGCTGGACCCTGATCTGGGGTTTTCCTGTAGCTTA 1440

Qy       2374 AGCGGTGCCAACTGCTTAAGTGATTGTAGAATCAGTAAGGCTGGAAAAGACCACAGATCA 2433
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AGCGGTGCCAACTGCTTAAGTGATTGTAGAATCAGTAAGGCTGGAAAAGACCACAGATCA 1500

Qy       2434 TTAAGTCCAACTGTCAGCCCCATCCCCACCGCGCCCACTGTCACTCAGTGCCACATCCAC 2493
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTAAGTCCAACTGTCAGCCCCATCCCCACCGCGCCCACTGTCACTCAGTGCCACATCCAC 1560

Qy       2494 GCATTTCTTGAACATCTCCAGGGACAGTGACTCCACCCGTCACCAGCTGTGCTTCAGAGC 2553
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCATTTCTTGAACATCTCCAGGGACAGTGACTCCACCCGTCACCAGCTGTGCTTCAGAGC 1620

Qy       2554 AGGCAGGGTGACAGTCTCAGTGCCAGTTGCATCCTGCTGAAGAGCTTAACAGTGCAGTTT 2613
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AGGCAGGGTGACAGTCTCAGTGCCAGTTGCATCCTGCTGAAGAGCTTAACAGTGCAGTTT 1680

Qy       2614 AACAACGGACTGATTTGTTGATGTGGTTGCTGAATCAGTACGTTGAGATGTCACTAAACT 2673
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 AACAACGGACTGATTTGTTGATGTGGTTGCTGAATCAGTACGTTGAGATGTCACTAAACT 1740

Qy       2674 TTTTGGAGATTAATTTCAGGATGGAACACATTCTTAACCCTGAAACCAGCCTTTGATTTG 2733
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TTTTGGAGATTAATTTCAGGATGGAACACATTCTTAACCCTGAAACCAGCCTTTGATTTG 1800

Qy       2734 GGCTTGGCATTTGCAGAATTTGCAGGAAAAGATTGTTTGGGAACAGATGAATGGAATTTC 2793
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GGCTTGGCATTTGCAGAATTTGCAGGAAAAGATTGTTTGGGAACAGATGAATGGAATTTC 1860

Qy       2794 CACCAAACAGAAAATTAACACTTACACCAGTTTGAGTCTGGTCTTCGTTCGATATTTCTT 2853
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CACCAAACAGAAAATTAACACTTACACCAGTTTGAGTCTGGTCTTCGTTCGATATTTCTT 1920

Qy       2854 AAGAATCTCATCATCCTCCCTGCTCTTGGACCAGTGCTGCTGACAGGAGGTGGAGGATCA 2913
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AAGAATCTCATCATCCTCCCTGCTCTTGGACCAGTGCTGCTGACAGGAGGTGGAGGATCA 1980

Qy       2914 TCAGGGTCAGCATCCTCAGCATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGA 2973
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TCAGGGTCAGCATCCTCAGCATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGA 2040

Qy       2974 GAACTGCTTTGATTCCCCAGGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCT 3033
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GAACTGCTTTGATTCCCCAGGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCT 2100

Qy       3034 GAAAGTCCAACTTTCTGAACTTCCAGCACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGG 3093
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GAAAGTCCAACTTTCTGAACTTCCAGCACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGG 2160

Qy       3094 CCACAGGGACTGTAGCCAGGCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGT 3153
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CCACAGGGACTGTAGCCAGGCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGT 2220

Qy       3154 GGCTGGGAGGCAGCTCT 3170
              |||||||||||||||||
Db       2221 GGCTGGGAGGCAGCTCT 2237
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RESULT 3
US-09-861-101-3
; Sequence 3, Application US/09861101
; Publication No. US20030018984A1
; GENERAL INFORMATION:
; APPLICANT: COLEMAN, MICHAEL
; SCHWARTZ, ROBERT
; DEMAYO, FRANCESCO J.
; TITLE OF INVENTION: IGF-1 EXPRESSION SYSTEM AND
; METHODS OF USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861,101
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,572
; FILING DATE: November 19, 1997
; APPLICATION NUMBER: 60/031,539
; FILING DATE: December 2, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/185-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-861-101-3

Query Match 40.9%; Score 2218; DB 3; Length 3599;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2224; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
              |||   |||  |     ||||||||||||||||||||||||||||||||||||||||||||
Db          3 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 62

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 122
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Qy      3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       123 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 182

Qy      3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       183 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 242

Qy      3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       243 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 302

Qy      3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       303 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 362

Qy      3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       363 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 422

Qy      3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       423 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 482

Qy      3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       483 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 542

Qy      3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       543 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 602

Qy      3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       603 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 662

Qy      3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       663 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 722

Qy      3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       723 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 782

Qy      3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       783 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 842

Qy      4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       843 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 902

Qy      4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       903 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 962

Qy      4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       963 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 1022

Qy      4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1023 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 1082

Qy      4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1083 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 1142

Qy      4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1143 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 1202

Qy      4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1203 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 1262

Qy      4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1263 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 1322

Qy      4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1323 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 1382

Qy      4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1383 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 1442

Qy      4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
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Db      1443 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 1502

Qy      4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
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Db      1503 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 1562

Qy      4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1563 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 1622

Qy      4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1623 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 1682

Qy      4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1683 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 1742

Qy      4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1743 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 1802

Qy      4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1803 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 1862

Qy      5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1863 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 1922

Qy      5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1923 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 1982

Qy      5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1983 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 2042

Qy      5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2043 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 2102

Qy      5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2103 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 2162

Qy      5350 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 5409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2163 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 2222

Qy      5410 GGCGAATTGGAGCT 5423
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Db      2223 GGCGAATTGGAGCT 2236
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RESULT 4
US-10-798-896-2
; Sequence 2, Application US/10798896
; Publication No. US20050238624A1
; GENERAL INFORMATION:
;  APPLICANT: ADViSYS, Inc.
;  TITLE OF INVENTION: Insulin-Like Growth Factor ("IGF-I") Plasmid Mediated Supplementa
;  TITLE OF INVENTION:  Therapeutic Applications
;  FILE REFERENCE: 108328.00172 - AVSI-0034
;  CURRENT APPLICATION NUMBER: US/10/798,896
;  CURRENT FILING DATE:  2004-03-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 3803
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleic acid sequence for the pAV2002 plasmid.
US-10-798-896-2

  Query Match             40.9%;  Score 2218;  DB 9;  Length 3803;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2224;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             |||   |||  |     ||||||||||||||||||||||||||||||||||||||||||||
Db       1570 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1629

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1689

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1749

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1750 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1809

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1810 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1869

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1870 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1929

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1930 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1989

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
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Db       1990 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 2049

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2050 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 2109

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2110 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 2169

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2170 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2229

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2230 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 2289

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
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Db       2290 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 2349

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2409

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2469

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2529

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2589

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2590 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2649

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2709

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2769

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2770 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2829

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2830 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2889

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
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Db       2890 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2949

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2950 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 3009

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
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Db       3010 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 3069

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 3129

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 3189

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3190 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 3249

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3309

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
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Db       3310 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 3369

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
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Db       3370 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3429

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3430 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3489

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3490 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3549

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3550 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3609

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3610 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3669

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3670 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3729

Qy       5350 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 5409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3730 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 3789

Qy       5410 GGCGAATTGGAGCT 5423
              ||||||||||||||
Db       3790 GGCGAATTGGAGCT 3803


RESULT 5
US-09-861-101-2
; Sequence 2, Application US/09861101
; Publication No. US20030018984A1
;   GENERAL INFORMATION:
;        APPLICANT: COLEMAN, MICHAEL
;                   SCHWARTZ, ROBERT
;                   DEMAYO, FRANCESCO J.
;        TITLE OF INVENTION: IGF-1 EXPRESSION SYSTEM AND
;                            METHODS OF USE
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/861,101
;             FILING DATE: 18-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/974,572
;             FILING DATE: November 19, 1997
;             APPLICATION NUMBER: 60/031,539
;             FILING DATE: December 2, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 230/185-PCT
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 3600 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-861-101-2

  Query Match             40.9%;  Score 2215.8;  DB 3;  Length 3600;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2217;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3205 CTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAG 3264
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 CCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAG 78

Qy       3265 CTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGC 3324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 CTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGC 138

Qy       3325 ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGC 3384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGC 198

Qy       3385 TCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA 3444
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA 258

Qy       3445 CGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG 3504
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG 318

Qy       3505 CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG 3564
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG 378

Qy       3565 TTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG 3624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 TTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG 438

Qy       3625 GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC 3684
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC 498

Qy       3685 GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA 3744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA 558

Qy       3745 TACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTT 3804
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Db        559 TACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTT 618

Qy       3805 ACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC 3864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC 678

Qy       3865 TGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC 3924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 TGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC 738

Qy       3925 CCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA 3984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 CCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA 798

Qy       3985 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT 4044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT 858

Qy       4045 GTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA 4104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        859 GTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACA 918
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Qy       4105 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT 4164
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Db        919 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT 978

Qy       4165 TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATT 4224
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATT 1038

Qy       4225 ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCT 4284
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCT 1098

Qy       4285 CAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATA 4344
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATA 1158

Qy       4345 CCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGG 4404
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGG 1218

Qy       4405 GTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAAT 4464
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Db       1219 GTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAAT 1278

Qy       4465 CCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACG 4524
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Db       1279 CCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACG 1338

Qy       4525 ACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCG 4584
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Db       1339 ACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCG 1398

Qy       4585 AGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTA 4644
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 AGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTA 1458

Qy       4645 CGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGC 4704
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 CGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGC 1518

Qy       4705 GTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGA 4764
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Db       1519 GTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGA 1578

Qy       4765 GATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCA 4824
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 GATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCA 1638

Qy       4825 GTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGC 4884
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 GTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGC 1698

Qy       4885 GCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACC 4944
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 GCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACC 1758

Qy       4945 GGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGT 5004
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 GGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGT 1818

Qy       5005 GCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCA 5064
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 GCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCA 1878

Qy       5065 TCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTG 5124
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1879 TCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTG 1938

Qy       5125 CGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACC 5184
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Db       1939 CGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACC 1998

Qy       5185 TTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAG 5244
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1999 TTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAG 2058

Qy       5245 TCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCG 5304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2059 TCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCG 2118

Qy       5305 AAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGA 5364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2119 AAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGA 2178

Qy       5365 CGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGAGCT 5423
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Db       2179 CGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGAGCT 2237
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RESULT 6
US-10-281-067B-26
; Sequence 26, Application US/10281067B
; Publication No. US20040138111A1
; GENERAL INFORMATION:
; APPLICANT: Baylor College of Medicine
; TITLE OF INVENTION: A COMPOSITION AND METHOD TO ALTER LEAN BODY MASS AND BOND PROPERTI
; TITLE OF INVENTION: SUBJECT
; FILE REFERENCE: 108328.00071 - AVSI-0008
; CURRENT APPLICATION NUMBER: US/10/281,067B
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 3558
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the inducible pGR1774 containing GHRH.
US-10-281-067B-26

Query Match 40.8%; Score 2211.6; DB 7; Length 3558;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2217; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
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Db       1200 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1259

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1260 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1319

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1379

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
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Db       1380 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1439

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Db       1440 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1499

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
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Db       1500 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1559

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
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Db       1560 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1619

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
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Db       1620 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1679
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Qy       3670 CTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
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Db       1680 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1739

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
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Db       1740 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1799

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
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Db       1800 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 1859

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
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Db       1860 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 1919

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
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Db       1920 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 1979

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
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Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
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Db       2040 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2099

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
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Db       2100 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2159

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
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Db       2160 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2219

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
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Db       2220 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2279

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
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Db       2280 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2339

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
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Db       2340 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2399

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2400 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2459

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
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Db       2460 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2519

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2520 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2579

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
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Db       2580 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2639

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
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Db       2640 GCTTCCATYCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2699

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2700 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2759

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2760 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2819

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
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Db       2820 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 2879

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
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Db       2880 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 2939

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
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Db       2940 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 2999

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
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Db       3000 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3059

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3060 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3119

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
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Db       3120 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3179

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
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Db       3180 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3239

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
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Db       3240 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3299

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3300 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3359

Qy       5350 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 5409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3360 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 3419

Qy       5410 GGCGAATT 5417
             ||||||||
Db       3420 GGCGAATT 3427
```

RESULT 7
US-10-764-818A-26
; Sequence 26, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADViSYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES
; TITLE OF INVENTION: CULLING IN HERD ANIMALS
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10/764,818A
; CURRENT FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 3558
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the inducible pGR1774 with human GHRH
US-10-764-818A-26

Query Match 40.8%; Score 2211.6; DB 8; Length 3558;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2217; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

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Qy      3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             |||   |||   |     ||||||||||||||||||||||||||||||||||||||||||
Db      1200 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1259

Qy      3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1260 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1319

Qy      3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1320 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1379

Qy      3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1380 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1439

Qy      3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1440 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1499

Qy      3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1500 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1559

Qy      3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1560 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1619

Qy      3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1620 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1679

Qy      3670 CTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1680 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1739

Qy      3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1740 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1799

Qy      3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1800 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 1859

Qy      3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1860 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 1919

Qy      3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1920 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 1979

Qy      3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1980 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2039

Qy      4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2040 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2099

Qy      4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2100 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2159

Qy      4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2160 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2219

Qy      4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2220 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2279

Qy      4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2280 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2339

Qy      4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2340 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2399

Qy      4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2400 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2459

Qy      4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2460 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2519

Qy      4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2520 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2579

Qy      4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2580 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2639

Qy      4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
             ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2640 GCTTCCATYCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2699

Qy      4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2700 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2759

Qy      4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2760 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2819

Qy      4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2820 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 2879

Qy      4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2880 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 2939

Qy      4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2940 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 2999

Qy      4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3000 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3059

Qy      5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3060 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3119

Qy      5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3120 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3179

Qy      5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3180 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3239

Qy      5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3240 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3299

Qy      5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3300 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3359

Qy      5350 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 5409
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3360 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 3419

Qy       5410 GGCGAATT 5417
                ||||||||
Db       3420 GGCGAATT 3427


RESULT 8
US-10-021-403A-10
; Sequence 10, Application US/10021403A
; Publication No. US20030074679A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys
;  TITLE OF INVENTION: Administration of Nucleic Acid Sequence to Female Animal to Enhan
;  TITLE OF INVENTION:  Growth in Offspring
;  FILE REFERENCE: HO-P02021US1/100021476/OTA 00-91
;  CURRENT APPLICATION NUMBER: US/10/021,403A
;  CURRENT FILING DATE:  2002-04-11
;  PRIOR APPLICATION NUMBER: 60/255,021
;  PRIOR FILING DATE: 2000-12-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 2192
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: This is a plasmid vector comprising a pVC0289 backbone
US-10-021-403A-10

  Query Match             39.8%;  Score 2160;  DB 5;  Length 2192;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 2166;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
                |||   |||   |     ||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 76

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 136

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 196

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 256

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 316

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 376

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 436

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 496

Qy       3670 CTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 556

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        557 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 616

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 676

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 736

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 796

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 856

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 916

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 976

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 1036

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 1096

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 1156

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1157 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 1216

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1217 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 1276

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1277 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 1336

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1337 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 1396

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1397 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 1456

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1457 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 1516

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1517 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 1576

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1577 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 1636

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1637 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 1696
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Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1697 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 1756

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1757 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 1816

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1817 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 1876

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1877 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 1936

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1937 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 1996

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1997 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 2056

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2057 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 2116

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2117 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 2176

Qy       5350 TTTTCCCAGTCACGAC 5365
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Db       2177 TTTTCCCAGTCACGAC 2192


RESULT 9
US-10-021-403A-9
; Sequence 9, Application US/10021403A
; Publication No. US20030074679A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys
;  TITLE OF INVENTION: Administration of Nucleic Acid Sequence to Female Animal to Enhan
;  TITLE OF INVENTION:  Growth in Offspring
;  FILE REFERENCE: HO-P02021US1/100021476/OTA 00-91
;  CURRENT APPLICATION NUMBER: US/10/021,403A
;  CURRENT FILING DATE:  2002-04-11
;  PRIOR APPLICATION NUMBER: 60/255,021
;  PRIOR FILING DATE: 2000-12-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 3534
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: This is a plasmid pSPC5-12-HVGHRH utilized in the present inventi
;   OTHER INFORMATION: on.
US-10-021-403A-9

  Query Match             39.8%;  Score 2160;  DB 5;  Length 3534;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 2166;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             |||   |||  |     ||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1478

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1598

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1658

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1719 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1778

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1779 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1838

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1839 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1898

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1899 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1958

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1959 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2019 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 2078

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2079 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 2138

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2139 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2198

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2199 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2258

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2379 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2438

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2439 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2498

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2499 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2558
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Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
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Db       2559 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2618

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2619 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2678

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2679 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2738

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2739 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2798

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2799 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2858

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2859 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2918

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2919 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2978

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2979 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 3038

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3039 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3098

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3099 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 3158

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3159 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3218

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3219 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3278

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3279 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3338

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3339 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3398

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3399 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3458

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3459 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3518

Qy       5350 TTTTCCCAGTCACGAC 5365
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Db       3519 TTTTCCCAGTCACGAC 3534
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RESULT 10
US-10-395-709-11
; Sequence 11, Application US/10395709
; Publication No. US20040014645A1

```
; GENERAL INFORMATION:
;  APPLICANT: Advisys
;  TITLE OF INVENTION: INCREASED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VIVO BY THE POL
;  TITLE OF INVENTION:  GLUTAMATE ("PLG") SYSTEM
;  FILE REFERENCE: 108328.00115 - AVSI-0021P1
;  CURRENT APPLICATION NUMBER: US/10/395,709
;  CURRENT FILING DATE:  2003-03-24
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 3534
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence for the operatively linked components of the HV-GHRH pla
;   OTHER INFORMATION: smid.
US-10-395-709-11
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Query Match 39.8%; Score 2160; DB 7; Length 3534;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
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Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1478

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1598

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1658

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1719 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1778

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1779 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1838

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1839 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1898

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1899 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1958

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1959 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2019 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 2078

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
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Db       2079 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 2138
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Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2139 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2198

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
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Db       2199 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2258

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
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Db       2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2379 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2438

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2439 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2498

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2499 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2558

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2559 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2618

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2619 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2678

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2679 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2738

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2739 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2798

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2799 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2858

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
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Db       2859 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2918

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
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Db       2919 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2978

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
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Db       2979 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 3038

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
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Db       3039 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3098

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
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Db       3099 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 3158

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3159 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3218

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3219 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3278

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3279 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3338

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3339 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3398

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3399 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3458

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3459 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3518

Qy       5350 TTTTCCCAGTCACGAC 5365
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Db       3519 TTTTCCCAGTCACGAC 3534
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RESULT 11
US-10-395-709-12
; Sequence 12, Application US/10395709
; Publication No. US20040014645A1
; GENERAL INFORMATION:
; APPLICANT: Advisys
; TITLE OF INVENTION: INCREASED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VIVO BY THE POL
; TITLE OF INVENTION: GLUTAMATE ("PLG") SYSTEM
; FILE REFERENCE: 108328.00115 - AVSI-0021P1
; CURRENT APPLICATION NUMBER: US/10/395,709
; CURRENT FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the operatively linked components of the TI-GHRH pla
; OTHER INFORMATION: smid.
US-10-395-709-12

Query Match 39.8%; Score 2160; DB 7; Length 3534;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
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Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
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Db       1419 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1478

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
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Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1598

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1658

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
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Db       1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1719 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1778

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1779 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1838

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
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Db       1839 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1898

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
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Db       1899 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1958

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1959 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
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Db       2019 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 2078

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
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Db       2079 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 2138

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2139 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2198

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
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Db       2199 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2258

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
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Db       2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
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Db       2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2379 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2438

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
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Db       2439 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2498

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
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Db       2499 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2558

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
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Db       2559 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2618

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
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Db       2619 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2678

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
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Db       2679 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2738

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
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Db       2739 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2798

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
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Db       2799 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2858

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2859 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2918

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2919 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2978

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2979 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 3038

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3039 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3098

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3099 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 3158

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3159 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3218

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
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Db       3219 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3278

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
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Db       3279 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3338

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
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Db       3339 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3398

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
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Db       3399 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3458

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
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Db       3459 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3518

Qy       5350 TTTTCCCAGTCACGAC 5365
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Db       3519 TTTTCCCAGTCACGAC 3534
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RESULT 12
US-10-395-709-13
; Sequence 13, Application US/10395709
; Publication No. US20040014645A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys
;  TITLE OF INVENTION: INCREASED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VIVO BY THE POL
;  TITLE OF INVENTION:  GLUTAMATE ("PLG") SYSTEM
;  FILE REFERENCE: 108328.00115 - AVSI-0021P1
;  CURRENT APPLICATION NUMBER: US/10/395,709
;  CURRENT FILING DATE:  2003-03-24
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 3534
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence for the operatively linked components of the TV-GHRH pla
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; OTHER INFORMATION: smid.
US-10-395-709-13

Query Match 39.8%; Score 2160; DB 7; Length 3534;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
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Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1478

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
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Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
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Db       1539 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1598

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
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Db       1599 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1658

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
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Db       1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
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Db       1719 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1778

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Db       1779 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1838

Qy       3670 CTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
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Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
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Db       1899 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1958

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
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Db       1959 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
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Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
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Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
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Db       2199 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2258

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
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Db       2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
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Db       2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378

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Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
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Db       2439 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2498

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
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Db       2499 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2558

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
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Db       2559 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2618

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
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Db       2619 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2678

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
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Db       2679 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2738

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
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Db       2739 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2798

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
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Db       2799 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2858

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2859 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2918

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2919 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2978

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2979 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 3038

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3039 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3098

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3099 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 3158

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3159 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3218

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3219 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3278

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3279 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3338

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3339 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3398

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3399 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3458
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Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3459 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3518

Qy       5350 TTTTCCCAGTCACGAC 5365
             ||||||||||||||||
Db       3519 TTTTCCCAGTCACGAC 3534


RESULT 13
US-10-395-709-14
; Sequence 14, Application US/10395709
; Publication No. US20040014645A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys
;  TITLE OF INVENTION: INCREASED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VIVO BY THE POL
;  TITLE OF INVENTION:  GLUTAMATE ("PLG") SYSTEM
;  FILE REFERENCE: 108328.00115 - AVSI-0021P1
;  CURRENT APPLICATION NUMBER: US/10/395,709
;  CURRENT FILING DATE:  2003-03-24
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 3534
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence for the operatively linked components of the 15/27/28 GH
;   OTHER INFORMATION: RH plasmid.
US-10-395-709-14

  Query Match             39.8%;  Score 2160;  DB 7;  Length 3534;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 2166;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             |||   |||  |      ||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1478

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1598

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1658

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1719 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1778

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1779 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1838

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1839 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1898

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1899 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1958

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1959 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2019 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 2078

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2079 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 2138

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2139 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2198

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2199 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2258

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2379 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2438

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2439 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2498

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2499 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2558

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2559 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2618

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2619 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2678

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2679 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2738

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2739 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2798

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2799 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2858

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2859 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2918

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2919 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2978

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2979 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 3038

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3039 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3098

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3099 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 3158

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3159 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3218

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3219 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3278

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3279 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3338

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3339 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3398

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3399 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3458

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3459 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3518

Qy       5350 TTTTCCCAGTCACGAC 5365
             ||||||||||||||||
Db       3519 TTTTCCCAGTCACGAC 3534


RESULT 14
US-10-395-709-15
; Sequence 15, Application US/10395709
; Publication No. US20040014645A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys
;  TITLE OF INVENTION: INCREASED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VIVO BY THE POL
;  TITLE OF INVENTION:  GLUTAMATE ("PLG") SYSTEM
;  FILE REFERENCE: 108328.00115 - AVSI-0021P1
;  CURRENT APPLICATION NUMBER: US/10/395,709
;  CURRENT FILING DATE:  2003-03-24
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 3534
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: This is the entire plasmid sequence for wildtype GHRH.
US-10-395-709-15

  Query Match             39.8%;  Score 2160;  DB 7;  Length 3534;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 2166;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             |||   |||  |      ||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1478

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1598

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1658

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1719 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1778

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1779 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1838

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1839 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1898

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1899 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1958

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1959 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2019 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 2078

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2079 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 2138

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2139 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2198

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2199 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2258

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2379 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2438

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2439 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2498

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2499 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2558

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
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Db       2559 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2618

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2619 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2678

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
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Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
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Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
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Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
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Db       2859 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2918

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
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Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
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Db       2979 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 3038

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
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Db       3039 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3098

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
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Db       3099 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 3158

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
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Db       3159 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3218

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
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Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
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Db       3519 TTTTCCCAGTCACGAC 3534


RESULT 15
US-10-359-919A-11
; Sequence 11, Application US/10359919A
; Publication No. US20040038918A1
; GENERAL INFORMATION:
;  APPLICANT: Baylor College of Medicine
;  TITLE OF INVENTION: Modified Pituitary Gland Development in offspring from Expectant M
;  TITLE OF INVENTION:  animals treated with GHRH
;  FILE REFERENCE: 108328.00087 - AVSI-0019
;  CURRENT APPLICATION NUMBER: US/10/359,919A
;  CURRENT FILING DATE:  2003-02-06
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 3534
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleic acid sequence of the HV-GHRH plasmid.
US-10-359-919A-11

  Query Match             39.8%;  Score 2160;  DB 7;  Length 3534;
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  Matches 2166;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

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Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
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Db       1899 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1958

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
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Job time : 3654 secs

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 19:23:14 ; Search time 1288 Seconds
(without alignments)
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Title: US-10-798-896-1
Perfect score: 5423
Sequence: 1 ccaccgcggtggcggccgtc.....ctatagggcgaattggagct 5423

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2160	39.8	3534	12	US-11-186-282-22	Sequence 22, Appl
2	1773	32.7	2722	12	US-11-186-282-23	Sequence 23, Appl
3	1773	32.7	2725	12	US-11-186-282-24	Sequence 24, Appl
4	1771.4	32.7	2700	12	US-11-186-282-33	Sequence 33, Appl
5	1771.4	32.7	2716	12	US-11-186-282-27	Sequence 27, Appl
6	1771.4	32.7	2716	12	US-11-186-282-28	Sequence 28, Appl
7	1771.4	32.7	2716	12	US-11-186-282-29	Sequence 29, Appl
8	1771.4	32.7	2716	12	US-11-186-282-31	Sequence 31, Appl
9	1771.4	32.7	2721	12	US-11-186-282-26	Sequence 26, Appl
10	1771.4	32.7	2721	12	US-11-186-282-34	Sequence 34, Appl
11	1771.4	32.7	2725	12	US-11-186-282-25	Sequence 25, Appl
12	1771.4	32.7	2725	12	US-11-186-282-32	Sequence 32, Appl
13	1771.4	32.7	2739	12	US-11-186-282-30	Sequence 30, Appl
c 14	1372.8	25.3	2403	7	US-10-523-682-1	Sequence 1, Appli
c 15	1347.2	24.8	5181	12	US-11-094-484-3	Sequence 3, Appli
c 16	1128.8	20.8	5225	12	US-11-231-725-1	Sequence 1, Appli
17	1082.6	20.0	4968	12	US-11-145-532-19	Sequence 19, Appl
18	1082.6	20.0	5073	12	US-11-145-532-18	Sequence 18, Appl
c 19	1082.6	20.0	17402	12	US-11-193-750-8	Sequence 8, Appli
20	1082.2	20.0	8953	12	US-11-183-664-64	Sequence 64, Appl
c 21	1081.2	19.9	5094	12	US-11-024-251-28	Sequence 28, Appl
c 22	1081.2	19.9	5103	12	US-11-024-251-26	Sequence 26, Appl
c 23	1081.2	19.9	5766	12	US-11-024-251-34	Sequence 34, Appl
c 24	1081.2	19.9	5972	12	US-11-024-251-30	Sequence 30, Appl
c 25	1081.2	19.9	6197	12	US-11-024-251-32	Sequence 32, Appl
c 26	1080.6	19.9	11110	7	US-10-978-927-20	Sequence 20, Appl
c 27	1080.6	19.9	12263	7	US-10-978-927-19	Sequence 19, Appl
c 28	1080	19.9	3448	12	US-11-024-959-773	Sequence 773, App
c 29	1080	19.9	5534	12	US-11-024-959-776	Sequence 776, App
c 30	1080	19.9	7160	12	US-11-024-959-777	Sequence 777, App
c 31	1079.4	19.9	5001	12	US-11-214-613-40	Sequence 40, Appl
c 32	1079.4	19.9	5034	12	US-11-214-613-33	Sequence 33, Appl
c 33	1079.4	19.9	5164	12	US-11-214-613-36	Sequence 36, Appl
c 34	1079.4	19.9	5277	12	US-11-214-613-25	Sequence 25, Appl
c 35	1079.4	19.9	5295	12	US-11-214-613-38	Sequence 38, Appl
c 36	1079.4	19.9	5327	12	US-11-214-613-27	Sequence 27, Appl
c 37	1079.4	19.9	5337	12	US-11-214-613-19	Sequence 19, Appl
c 38	1079.4	19.9	5337	12	US-11-214-613-23	Sequence 23, Appl
c 39	1079.4	19.9	5337	12	US-11-214-613-31	Sequence 31, Appl
c 40	1079.4	19.9	5338	12	US-11-214-613-15	Sequence 15, Appl
c 41	1079.4	19.9	5338	12	US-11-214-613-29	Sequence 29, Appl
c 42	1079.4	19.9	5345	12	US-11-214-613-17	Sequence 17, Appl
c 43	1079.4	19.9	5387	12	US-11-214-613-41	Sequence 41, Appl
c 44	1079.4	19.9	5395	12	US-11-214-613-21	Sequence 21, Appl
c 45	1079.4	19.9	7239	12	US-11-089-551A-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-11-186-282-22
; Sequence 22, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Plasmid vector having an analog GHRH sequence.
US-11-186-282-22

Query Match 39.8%; Score 2160; DB 12; Length 3534;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             ||| ||| |     ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1478

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1598

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1658
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Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1719 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1778

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1779 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1838

Qy       3670 CTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1839 CTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1898

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1899 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1958

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1959 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2019 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 2078

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2079 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 2138

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2139 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2198

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2199 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2258

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2379 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2438

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2439 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2498

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2499 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2558

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2559 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2618

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2619 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2678

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2679 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2738

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2739 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2798

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2799 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2858

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2859 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2918

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2919 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2978

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2979 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 3038

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3039 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3098

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3099 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 3158

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3159 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3218

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3219 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3278

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3279 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3338

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3339 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3398

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3399 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3458

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3459 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3518

Qy       5350 TTTTCCCAGTCACGAC 5365
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Db       3519 TTTTCCCAGTCACGAC 3534
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RESULT 2
US-11-186-282-23
; Sequence 23, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: artificial sequence

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;   FEATURE:
;   OTHER INFORMATION: Plasmid vector having a codon optimized mouse GHRH sequence
US-11-186-282-23

  Query Match             32.7%;  Score 1773;  DB 12;  Length 2722;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1803;  Conservative    0;  Mismatches   15;  Indels   11;  Gaps    1;

Qy       3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
              || |  ||||    |   |   | ||||||||||||||||||||||||||||||||||||
Db        860 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 919

Qy       3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 979

Qy       3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1039

Qy       3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1040 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1099

Qy       3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1100 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1159

Qy       3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1160 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1219

Qy       3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1220 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1279

Qy       3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1280 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1339

Qy       3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1340 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1399

Qy       3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1400 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1459

Qy       4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1460 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1519

Qy       4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1520 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1579

Qy       4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1580 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 1639

Qy       4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA-----------CG 4282
              |||||||||||||||||||||||||||||||||||||||||||||||           ||
Db       1640 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1699

Qy       4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1759

Qy       4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1760 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1819

Qy       4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1820 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1879

Qy       4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1880 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1939

Qy       4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1940 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 1999

Qy       4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2000 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2059

Qy       4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2060 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2119

Qy       4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2120 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2179

Qy       4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2180 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2239

Qy       4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2240 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2299

Qy       4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2300 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2359

Qy       4943 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2360 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2419

Qy       5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2420 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2479

Qy       5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2480 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2539

Qy       5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2540 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2599

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2600 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2659

Qy       5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
              |||||||||||||||||||||||||||||
Db       2660 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2688

RESULT 3
US-11-186-282-24
; Sequence 24, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys, Inc.
;  TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
;  FILE REFERENCE: 108328.000265 AVSI-0042
;  CURRENT APPLICATION NUMBER: US/11/186,282
;  CURRENT FILING DATE:  2005-07-21
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
```

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;   LENGTH: 2725
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Plasmid vector having a codon optimized rat GHRH sequence
US-11-186-282-24

  Query Match            32.7%;  Score 1773;  DB 12;  Length 2725;
  Best Local Similarity  98.6%;  Pred. No. 0;
  Matches 1803;  Conservative    0;  Mismatches   15;  Indels   11;  Gaps    1;

Qy       3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
              ||  |  ||||    |   |   | ||||||||||||||||||||||||||||||||||||
Db        863 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 922

Qy       3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        923 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 982

Qy       3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1042

Qy       3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1043 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1102

Qy       3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1103 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1162

Qy       3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1163 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1222

Qy       3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1223 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1282

Qy       3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1283 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1342

Qy       3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1343 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1402

Qy       3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1403 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1462

Qy       4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1463 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1522

Qy       4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1523 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1582

Qy       4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1583 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 1642

Qy       4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA----------CG 4282
              ||||||||||||||||||||||||||||||||||||||||||||||          ||
Db       1643 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1702

Qy       4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1703 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1762

Qy       4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1763 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1822

Qy       4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1823 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1882

Qy       4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1883 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1942

Qy       4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1943 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 2002

Qy       4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2003 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2062

Qy       4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2063 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2122

Qy       4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2123 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2182

Qy       4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2183 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2242

Qy       4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2243 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2302

Qy       4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2303 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2362

Qy       4943 CCGGGCGCCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2363 CCGGGCGCCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2422

Qy       5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2423 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2482

Qy       5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2483 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2542

Qy       5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2543 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2602

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2603 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2662

Qy       5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
              |||||||||||||||||||||||||||||
Db       2663 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2691


RESULT 4
US-11-186-282-33
; Sequence 33, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys, Inc.
;  TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
;  FILE REFERENCE: 108328.000265 AVSI-0042
;  CURRENT APPLICATION NUMBER: US/11/186,282
;  CURRENT FILING DATE:  2005-07-21
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;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
;   LENGTH: 2700
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: This is the optimized plasmid for Horse GHRH.
US-11-186-282-33

  Query Match             32.7%;  Score 1771.4;  DB 12;  Length 2700;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1802;  Conservative    0;  Mismatches   16;  Indels   11;  Gaps    1;

Qy       3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
              ||  |  ||||     |   |    | ||||||||||||||||||||||||||||||||||
Db        859 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 918

Qy       3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 978

Qy       3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1038

Qy       3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1098

Qy       3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1158

Qy       3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1218

Qy       3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1278

Qy       3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1338

Qy       3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1398

Qy       3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1458

Qy       4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1518

Qy       4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1578

Qy       4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1579 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTACAAGCAGCAGATTACGCGCAGA 1638

Qy       4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA----------CG 4282
              ||||||||||||||||||||||||||||||||||||||||||||||          ||
Db       1639 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1698

Qy       4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1758

Qy       4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1818

Qy       4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1878

Qy       4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1879 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1938

Qy       4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 1998

Qy       4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1999 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2058

Qy       4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2059 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2118

Qy       4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2119 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2178

Qy       4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2179 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2238

Qy       4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2239 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2298

Qy       4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2299 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2358

Qy       4943 CCGGGCGCCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2359 CCGGGCGCCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2418

Qy       5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2419 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2478

Qy       5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2479 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2538

Qy       5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2539 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2598

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2599 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2658

Qy       5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
              |||||||||||||||||||||||||||||
Db       2659 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2687


RESULT 5
US-11-186-282-27
; Sequence 27, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys, Inc.
;  TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
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;  FILE REFERENCE: 108328.000265 AVSI-0042
;  CURRENT APPLICATION NUMBER: US/11/186,282
;  CURRENT FILING DATE:  2005-07-21
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
;   LENGTH: 2716
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: This is the codon optimized dog-GHRH expression plasmid.
US-11-186-282-27

  Query Match            32.7%;  Score 1771.4;  DB 12;  Length 2716;
  Best Local Similarity  98.5%;  Pred. No. 0;
  Matches 1802;  Conservative    0;  Mismatches   16;  Indels   11;  Gaps    1;

Qy       3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
             || |  ||||    |   |   | ||||||||||||||||||||||||||||||||||||
Db        854 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 913

Qy       3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 973

Qy       3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1033

Qy       3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1093

Qy       3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1153

Qy       3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1154 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1213

Qy       3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1214 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1273

Qy       3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1274 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1333

Qy       3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1334 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1393

Qy       3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1394 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1453

Qy       4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1454 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1513

Qy       4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1514 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1573

Qy       4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1574 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTACAAGCAGCAGATTACGCGCAGA 1633

Qy       4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA----------CG 4282
             ||||||||||||||||||||||||||||||||||||||||||||||||          ||
Db       1634 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1693
.

Qy       4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1694 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1753

Qy       4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1754 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1813

Qy       4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1814 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1873

Qy       4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1874 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1933

Qy       4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1934 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 1993

Qy       4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1994 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2053

Qy       4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2054 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2113

Qy       4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2114 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2173

Qy       4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2174 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2233

Qy       4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2234 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2293

Qy       4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2294 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2353

Qy       4943 CCGGGCGCCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2354 CCGGGCGCCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2413

Qy       5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2414 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2473

Qy       5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2474 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2533

Qy       5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2534 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2593

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2594 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2653

Qy       5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
             |||||||||||||||||||||||||||||
Db       2654 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2682


RESULT 6
US-11-186-282-28
; Sequence 28, Application US/11186282
; Publication No. US20060025368A1
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; GENERAL INFORMATION:
;  APPLICANT: Advisys, Inc.
;  TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
;  FILE REFERENCE: 108328.000265 AVSI-0042
;  CURRENT APPLICATION NUMBER: US/11/186,282
;  CURRENT FILING DATE:  2005-07-21
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
;   LENGTH: 2716
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: This is the codon optimized bovine-GHRH expression plasmid.
US-11-186-282-28

  Query Match             32.7%;  Score 1771.4;  DB 12;  Length 2716;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1802;  Conservative    0;  Mismatches   16;  Indels   11;  Gaps    1;

Qy       3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
              ||  |  ||||     |   |   | ||||||||||||||||||||||||||||||||||||
Db        854 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 913

Qy       3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 973

Qy       3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1033

Qy       3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1093

Qy       3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1153

Qy       3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1154 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1213

Qy       3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1214 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1273

Qy       3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1274 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1333

Qy       3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1334 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1393

Qy       3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1394 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1453

Qy       4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1454 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1513

Qy       4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1514 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1573

Qy       4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1574 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTACAAGCAGCAGATTACGCGCAGA 1633

Qy       4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA----------CG 4282
              ||||||||||||||||||||||||||||||||||||||||||||||||||          ||
Db       1634 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1693

Qy       4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1694 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1753

Qy       4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1754 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1813

Qy       4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1814 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1873

Qy       4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1874 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1933

Qy       4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1934 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 1993

Qy       4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1994 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2053

Qy       4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2054 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2113

Qy       4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2114 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2173

Qy       4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2174 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2233

Qy       4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2234 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2293

Qy       4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2294 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2353

Qy       4943 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2354 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2413

Qy       5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2414 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2473

Qy       5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2474 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2533

Qy       5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2534 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2593

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2594 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2653

Qy       5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
              |||||||||||||||||||||||||||||
Db       2654 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2682

RESULT 7
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US-11-186-282-29
; Sequence 29, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys, Inc.
;  TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
;  FILE REFERENCE: 108328.000265 AVSI-0042
;  CURRENT APPLICATION NUMBER: US/11/186,282
;  CURRENT FILING DATE:  2005-07-21
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
;   LENGTH: 2716
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: This is the codon optimized cat-GHRH expression plasmid.
US-11-186-282-29

  Query Match             32.7%;  Score 1771.4;  DB 12;  Length 2716;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1802;  Conservative    0;  Mismatches   16;  Indels   11;  Gaps    1;

Qy       3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
              ||  |  ||||     |   |   | ||||||||||||||||||||||||||||||||||||
Db        854 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 913

Qy       3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 973

Qy       3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
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Db        974 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1033

Qy       3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1093

Qy       3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1153

Qy       3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1154 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1213

Qy       3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1214 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1273

Qy       3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1274 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1333

Qy       3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1334 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1393

Qy       3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1394 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1453

Qy       4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1454 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1513

Qy       4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1514 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1573

Qy       4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||

Db       1574 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTACAAGCAGCAGATTACGCGCAGA 1633

Qy       4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA----------CG 4282
              ||||||||||||||||||||||||||||||||||||||||||||||||||          ||
Db       1634 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1693

Qy       4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1694 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1753

Qy       4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1754 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1813

Qy       4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1814 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1873

Qy       4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1874 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1933

Qy       4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1934 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 1993

Qy       4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1994 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2053

Qy       4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2054 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2113

Qy       4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2114 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2173

Qy       4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2174 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2233

Qy       4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2234 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2293

Qy       4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2294 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2353

Qy       4943 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2354 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2413

Qy       5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2414 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2473

Qy       5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2474 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2533

Qy       5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2534 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2593

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2594 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2653

Qy       5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
              |||||||||||||||||||||||||||||
Db       2654 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2682
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RESULT 8
US-11-186-282-31
; Sequence 31, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized ovine-GHRH expression plasmid.
US-11-186-282-31

Query Match 32.7%; Score 1771.4; DB 12; Length 2716;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;

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Qy       3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
             || |  ||||    |   |   | ||||||||||||||||||||||||||||||||||||||
Db        854 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 913

Qy       3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 973

Qy       3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1033

Qy       3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1093

Qy       3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1153

Qy       3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1154 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1213

Qy       3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1214 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1273

Qy       3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1274 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1333

Qy       3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1334 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1393

Qy       3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1394 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1453

Qy       4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1454 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1513

Qy       4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1514 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1573

Qy       4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1574 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTACAAGCAGCAGATTACGCGCAGA 1633

Qy       4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA----------CG 4282
             ||||||||||||||||||||||||||||||||||||||||||||||||          ||
Db       1634 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1693

Qy       4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1694 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1753

Qy       4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1754 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1813

Qy       4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1814 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1873

Qy       4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1874 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1933

Qy       4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1934 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 1993

Qy       4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1994 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2053

Qy       4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2054 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2113

Qy       4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2114 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2173

Qy       4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2174 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2233

Qy       4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2234 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2293

Qy       4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2294 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2353

Qy       4943 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2354 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2413

Qy       5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2414 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2473

Qy       5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2474 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2533

Qy       5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2534 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2593

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2594 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2653
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Qy       5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
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Db       2654 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2682
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RESULT 9
US-11-186-282-26
; Sequence 26, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 2721
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized pig-GHRH expression plasmid.
US-11-186-282-26

Query Match 32.7%; Score 1771.4; DB 12; Length 2721;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;

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Qy       3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
             || |  ||||    |   |   | ||||||||||||||||||||||||||||||||||||
Db        859 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 918

Qy       3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 978

Qy       3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1038

Qy       3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1098

Qy       3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1158

Qy       3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1218

Qy       3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1278

Qy       3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1338

Qy       3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1398

Qy       3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1458

Qy       4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1518

Qy       4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1578

Qy       4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1579 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTACAAGCAGCAGATTACGCGCAGA 1638

Qy       4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA----------CG 4282
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Db       1639 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1698

Qy       4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1758

Qy       4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1818

Qy       4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1878

Qy       4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1879 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1938

Qy       4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 1998

Qy       4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1999 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2058

Qy       4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2059 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2118

Qy       4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2119 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2178

Qy       4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2179 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2238

Qy       4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2239 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2298

Qy       4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2299 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2358

Qy       4943 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2359 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2418

Qy       5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2419 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2478

Qy       5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2479 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2538

Qy       5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2539 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2598

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
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Db         2599 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2658

Qy         5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
                |||||||||||||||||||||||||||||
Db         2659 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2687
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RESULT 10
US-11-186-282-34
; Sequence 34, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
;   LENGTH: 2721
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: This is the codon optimized Human-GHRH expression plasmid.
US-11-186-282-34

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  Query Match             32.7%;  Score 1771.4;  DB 12;  Length 2721;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1802;  Conservative    0;  Mismatches   16;  Indels   11;  Gaps    1;

Qy         3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
                || |  ||||    |   |   | ||||||||||||||||||||||||||||||||||||
Db          859 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 918

Qy         3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          919 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 978

Qy         3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          979 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1038

Qy         3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1039 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1098

Qy         3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1099 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1158

Qy         3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1159 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1218

Qy         3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1219 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1278

Qy         3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1279 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1338

Qy         3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1339 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1398

Qy         3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1399 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1458

Qy         4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1459 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1518

Qy         4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1519 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1578

Qy         4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
                ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         1579 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTACAAGCAGCAGATTACGCGCAGA 1638

Qy         4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA-----------CG 4282
                |||||||||||||||||||||||||||||||||||||||||||||||           ||
Db         1639 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1698

Qy         4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1699 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1758

Qy         4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1759 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1818

Qy         4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1819 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1878

Qy         4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
                |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db         1879 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1938

Qy         4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1939 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 1998

Qy         4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1999 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2058

Qy         4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2059 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2118

Qy         4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2119 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2178

Qy         4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2179 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2238

Qy         4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2239 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2298

Qy         4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2299 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2358

Qy         4943 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2359 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2418

Qy         5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2419 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2478

Qy         5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2479 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2538

Qy         5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2539 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2598

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2599 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2658

Qy       5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
             |||||||||||||||||||||||||||||
Db       2659 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2687


RESULT 11
US-11-186-282-25
; Sequence 25, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys, Inc.
;  TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
;  FILE REFERENCE: 108328.000265 AVSI-0042
;  CURRENT APPLICATION NUMBER: US/11/186,282
;  CURRENT FILING DATE:  2005-07-21
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
;   LENGTH: 2725
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: This is the codon optimized HV-GHRH expression plasmid.
US-11-186-282-25

  Query Match             32.7%;  Score 1771.4;  DB 12;  Length 2725;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1802;  Conservative    0;  Mismatches   16;  Indels   11;  Gaps    1;

Qy       3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
             ||  |  ||||    |   |   | ||||||||||||||||||||||||||||||||||||
Db        863 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 922

Qy       3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        923 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 982

Qy       3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1042

Qy       3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1043 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1102

Qy       3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1103 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1162

Qy       3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1163 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1222

Qy       3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1223 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1282

Qy       3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1283 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1342

Qy       3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1343 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1402

Qy       3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
.

Db       1403 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1462

Qy       4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1463 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1522

Qy       4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1523 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1582

Qy       4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1583 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTACAAGCAGCAGATTACGCGCAGA 1642

Qy       4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA----------CG 4282
             |||||||||||||||||||||||||||||||||||||||||||||||          ||
Db       1643 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1702

Qy       4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1703 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1762

Qy       4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1763 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1822

Qy       4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1823 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1882

Qy       4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1883 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1942

Qy       4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1943 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 2002

Qy       4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2003 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2062

Qy       4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2063 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2122

Qy       4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2123 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2182

Qy       4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2183 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2242

Qy       4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2243 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2302

Qy       4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2303 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2362

Qy       4943 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2363 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2422

Qy       5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2423 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2482

Qy       5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2483 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2542
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Qy       5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2543 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2602

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2603 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2662

Qy       5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
             |||||||||||||||||||||||||||||
Db       2663 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2691


RESULT 12
US-11-186-282-32
; Sequence 32, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys, Inc.
;  TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
;  FILE REFERENCE: 108328.000265 AVSI-0042
;  CURRENT APPLICATION NUMBER: US/11/186,282
;  CURRENT FILING DATE:  2005-07-21
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
;   LENGTH: 2725
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: This is the codon optimized chicken-GHRH expression plasmid.
US-11-186-282-32

  Query Match             32.7%;  Score 1771.4;  DB 12;  Length 2725;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1802;  Conservative    0;  Mismatches   16;  Indels   11;  Gaps    1;

Qy       3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
             || |  ||||    |   |   | ||||||||||||||||||||||||||||||||||||
Db        863 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 922

Qy       3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        923 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 982

Qy       3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1042

Qy       3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1043 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1102

Qy       3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1103 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1162

Qy       3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1163 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1222

Qy       3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1223 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1282

Qy       3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1283 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1342

Qy       3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1343 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1402

Qy       3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1403 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1462

Qy       4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1463 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1522

Qy       4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1523 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1582

Qy       4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1583 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTACAAGCAGCAGATTACGCGCAGA 1642

Qy       4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA----------CG 4282
             ||||||||||||||||||||||||||||||||||||||||||||||          ||
Db       1643 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1702

Qy       4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1703 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1762

Qy       4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1763 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1822

Qy       4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1823 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1882

Qy       4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1883 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1942

Qy       4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1943 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 2002

Qy       4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2003 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2062

Qy       4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2063 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2122

Qy       4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2123 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2182

Qy       4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2183 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2242

Qy       4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2243 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2302

Qy       4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2303 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2362

Qy       4943 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2363 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2422

Qy       5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2423 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2482
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Qy       5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2483 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2542

Qy       5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2543 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2602

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2603 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2662

Qy       5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
             |||||||||||||||||||||||||||||
Db       2663 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2691


RESULT 13
US-11-186-282-30
; Sequence 30, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
;  APPLICANT: Advisys, Inc.
;  TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
;  FILE REFERENCE: 108328.000265 AVSI-0042
;  CURRENT APPLICATION NUMBER: US/11/186,282
;  CURRENT FILING DATE:  2005-07-21
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
;   LENGTH: 2739
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: This is the codon optimized TI-GHRH expression plasmid.
US-11-186-282-30

  Query Match            32.7%;  Score 1771.4;  DB 12;  Length 2739;
  Best Local Similarity  98.5%;  Pred. No. 0;
  Matches 1802;  Conservative    0;  Mismatches   16;  Indels   11;  Gaps    1;

Qy       3454 AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
             || |  ||||    |   |   | ||||||||||||||||||||||||||||||||||||||
Db        877 AGTGAGGGTTAATTTCGAGCTTGGTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 936

Qy       3514 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 3573
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA 996

Qy       3574 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        997 GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1056

Qy       3634 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 3693
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1057 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC 1116

Qy       3694 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 3753
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG 1176

Qy       3754 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 3813
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC 1236

Qy       3814 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1296

Qy       3874 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 3933
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1297 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG 1356

Qy       3934 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 3993
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1357 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC 1416

Qy       3994 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 4053
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1417 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1476

Qy       4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1477 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1536

Qy       4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1537 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1596

Qy       4174 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA 4233
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1597 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTACAAGCAGCAGATTACGCGCAGA 1656

Qy       4234 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA----------CG 4282
             ||||||||||||||||||||||||||||||||||||||||||||||||          ||
Db       1657 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1716

Qy       4283 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 4342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1717 CTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGA 1776

Qy       4343 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 4402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1777 TACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCAC 1836

Qy       4403 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 4462
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1837 GGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 1896

Qy       4463 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA 4522
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1897 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGAGTCA 1956

Qy       4523 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 4582
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1957 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCG 2016

Qy       4583 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 4642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2017 CGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAG 2076

Qy       4643 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 4702
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2077 TACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAA 2136

Qy       4703 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 4762
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2137 GCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 2196

Qy       4763 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 4822
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2197 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT 2256

Qy       4823 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 4882
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2257 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCC 2316

Qy       4883 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 4942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2317 GCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAA 2376

Qy       4943 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 5002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2377 CCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTT 2436

Qy       5003 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 5062
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Db       2437 GTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATC 2496

Qy       5063 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 5122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2497 CATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC 2556

Qy       5123 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 5182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2557 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAA 2616

Qy       5183 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 5242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2617 CCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCC 2676

Qy       5243 AGTCTAGCAACTGTTGGGAAGGGCGATCG 5271
             |||||||||||||||||||||||||||||
Db       2677 AGTCTAGCAACTGTTGGGAAGGGCGATCG 2705


RESULT 14
US-10-523-682-1/c
; Sequence 1, Application US/10523682
; Publication No. US20060014149A1
; GENERAL INFORMATION:
;  APPLICANT: Schnorr, Kirk
;  TITLE OF INVENTION: Methods for rolling circle amplification and signal trapping of
;  TITLE OF INVENTION:  libraries
;  FILE REFERENCE: 10292.204-US
;  CURRENT APPLICATION NUMBER: US/10/523,682
;  CURRENT FILING DATE:  2005-02-01
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 2403
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Plasmid pMHas5
US-10-523-682-1

  Query Match            25.3%;  Score 1372.8;  DB 7;  Length 2403;
  Best Local Similarity  82.4%;  Pred. No. 0;
  Matches 1759;  Conservative    0;  Mismatches  172;  Indels  203;  Gaps    8;

Qy       3269 TTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAA 3328
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2193 TTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAA 2134

Qy       3329 AGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCAC 3388
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2133 AGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCAC 2074

Qy       3389 TGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCG 3448
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2073 TGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCG 2014

Qy       3449 CGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGC 3508
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2013 CGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGC 1954

Qy       3509 GCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTAT 3568
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1953 GCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTAT 1894

Qy       3569 CCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA 3628
             ||||||||||||||||||||||||||||||||
Db       1893 CCACAGAATCAGGGGATAACGCAGGAAAGAA---------------------------- 1863

Qy       3629 GGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGC 3688
                          |     | ||||||||||||||||||||||||||||||||||| |||
Db       1862 ------------------GGCAAAGCCGTTTTTCCATAGGCTCCGCCCCCCTGACAAGC 1822
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Qy       3689 ATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACC 3748
             ||||| |||   |||||||||| |||| ||||||||||||||||||||||||||||||||||
Db       1821 ATCACGAAATCTGACGCTCAAATCAGTGGTGGCGAAACCCGACAGGACTATAAAGATACC 1762

Qy       3749 AGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCG 3808
             |||||||| |||||||  |||||||||||||||||||||||||   || | | | ||||||
Db       1761 AGGCGTTT-CCCCTGGCGGCTCCCTCGTGCGCTCTCCTGTTCCTGCCTTTCGGTTTACCG 1703

Qy       3809 GATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTA 3868
             |           | || | |  ||  ||  ||||    ||    ||    ||
Db       1702 G--------TGTCATTCCGCTGTTATGGCCGCGTTTGTCTCATTCCACGC---------C 1660

Qy       3869 GGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCG 3928
              |   ||||||||  | |||||  ||||||||||||||| |||| ||||||||||||||||
Db       1659 TGACACTCAGTTCCGGGTAGGCAGTTCGCTCCAAGCTGGACTGTATGCACGAACCCCCCG 1600

Qy       3929 TTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGAC 3988
             |||||  |||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db       1599 TTCAGTCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGAAAGAC 1540

Qy       3989 ACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAG 4048
              | |    | | ||||||||||||||||||||||||  |  ||||  |||  ||
Db       1539 ATGCAAAAGCACCACTGGCAGCAGCCACTGGTAATTGATTTAGAGGAGTTAG-------- 1488

Qy       4049 GCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTAT 4108
                                 |||||||||  ||  |    || ||||| |||  ||| |
Db       1487 ---------------TCTTGAAGTCATGCGCCGGTTAAGGCTAAACTGAAAGGACAAGTT 1443

Qy       4109 TTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGAT 4168
              |||||  ||||||||  |  |||||||||||||  |   ||||||||||||||||
Db       1442 TTGGTGACTGCGCTCCTC-CAAGCCAGTTACCTCGGTTCAAAGAGTTGGTAGCTCAGAGA 1384

Qy       4169 CCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGC 4228
              |    | |||||  ||          |||||  |||||  |||  ||||  |||||||||
Db       1383 ACCTTCGAAAAACCGCCCTGCAAGGCGGT--TTTTTCGTTTTCAGAGCAAGAGATTACGC 1326

Qy       4229 GCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTA------------------ 4270
              |||||  ||||  |||||||||||||||  | | ||   |   |
Db       1325 GCAGACCAAAACGATCTCAAGAAGATCATCTTATTAATCAGATAAAATATTTCTAGATTT 1266

Qy       4271 ---------------------------------------------------------- 4270

Db       1265 CAGTGCAATTTATCTCTTCAAATGTAGCACCTGAAGTCAGCCCCATACGATATAAGTTGT 1206

Qy       4271 --------------------------------CGGGGTCTGACGCTCAGAAGAACTCGT 4297
                                               |  |  | ||||||||||||||||||
Db       1205 AATTCTCATGTTTGACAGCTTATCATCGCGAACCCCAGAGTCCCGCTCAGAAGAACTCGT 1146

Qy       4298 CAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGA 4357
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1145 CAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGA 1086

Qy       4358 GGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTA 4417
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1085 GGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTA 1026

Qy       4418 TGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGC 4477
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1025 TGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGC 966

Qy       4478 CATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGC 4537
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        965 CATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGC 906

Qy       4538 CGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCT 4597
             |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        905 CGTCGGGCATCCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCT 846

Qy       4598 CTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGA 4657
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Db        785 TGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCC 726

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Db        725 GCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGAT 666

Qy       4778 CCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGA 4837
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             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| | | |
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RESULT 15
US-11-094-484-3/c
; Sequence 3, Application US/11094484
; Publication No. US20050261231A1
; GENERAL INFORMATION:
; APPLICANT: KUBO, TATEKI
; APPLICANT: TANAG, MARVIN A.
; APPLICANT: YANO, KENJI
; APPLICANT: HOSOKAWA, KO
; APPLICANT: MORISHITA, RYUICHI
; TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR NUCLEIC ACID SEQUENCE TO
; TITLE OF INVENTION: ENHANCE MUSCULOCUTANEOUS FLAP SURVIVAL
; FILE REFERENCE: 074257-0108
; CURRENT APPLICATION NUMBER: US/11/094,484
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: 60/557,835
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 5181
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: vector sequence
US-11-094-484-3

Query Match 24.8%; Score 1347.2; DB 12; Length 5181;

Best Local Similarity 84.9%; Pred. No. 0;
Matches 1648; Conservative 0; Mismatches 3; Indels 289; Gaps 1;

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Qy       3715 AGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTC 3774
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Qy       3775 GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCG 3834
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Qy       3835 GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT 3894
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Qy       4626 ACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGG 4685
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Search completed: February 20, 2006, 19:49:16
Job time : 1300 secs

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 18:48:03 ; Search time 25985 Seconds
(without alignments)
11863.076 Million cell updates/sec

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Perfect score: 5423
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
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7: gb_ph:*
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11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	2237	41.3	2237	6	CQ877114	CQ877114 Sequence
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4	2218	40.9	3599	6	BD069041	BD069041 Treatment
5	2218	40.9	3803	6	CQ877111	CQ877111 Sequence
6	2215.8	40.9	3600	6	BD063789	BD063789 Insulin-l
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9	2160	39.8	3534	6	CQ854723	CQ854723 Sequence
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12	2160	39.8	3534	6	CQ854726	CQ854726 Sequence
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO2004081040.
ACCESSION CQ877110
VERSION CQ877110.1 GI:53790386
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Rabinovsky,E.D. and Draghia-Akli,R.
TITLE Insulin-like growth factor (igf-i) plasmid-mediated supplementation for therapeutic applications
JOURNAL Patent: WO 2004081040-A 1 23-SEP-2004;
Advisys, Inc. (US); BAYLOR COLLEGE OF MEDICINE (US)
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/note="Nucleic acid sequence for the pAV2001 plasmid."
ORIGIN

Query Match 100.0%; Score 5423; DB 6; Length 5423;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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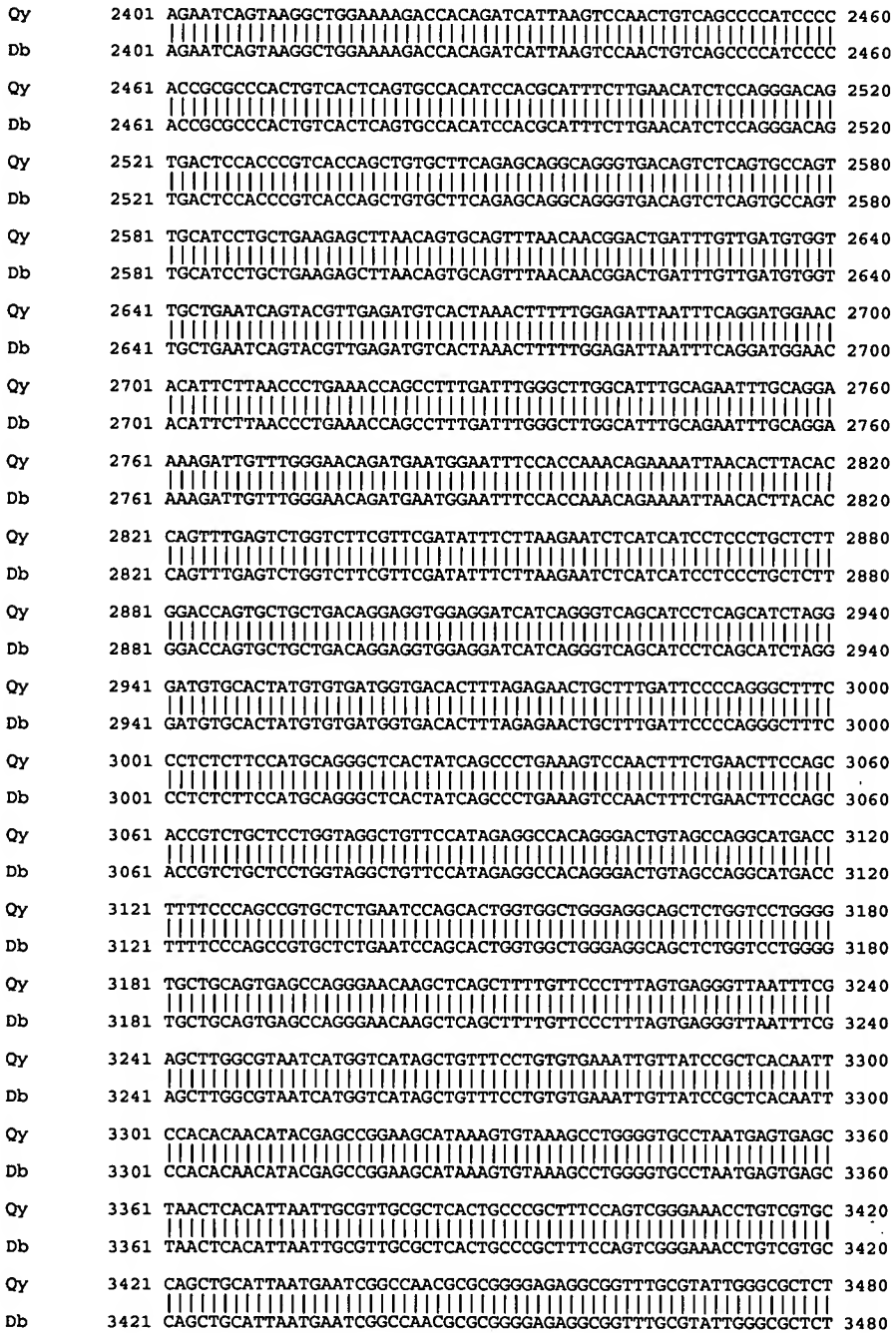
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REFERENCE   1
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Db       1921 AAGAATCTCATCATCCTCCCTGCTCTTGGACCAGTGCTGCTGACAGGAGGTGGAGGATCA 1980

Qy       2914 TCAGGGTCAGCATCCTCAGCATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGA 2973

Db       1981 TCAGGGTCAGCATCCTCAGCATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGA 2040

Qy       2974 GAACTGCTTTGATTCCCCAGGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCT 3033

Db       2041 GAACTGCTTTGATTCCCCAGGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCT 2100

Qy       3034 GAAAGTCCAACTTTCTGAACTTCCAGCACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGG 3093

Db       2101 GAAAGTCCAACTTTCTGAACTTCCAGCACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGG 2160

Qy       3094 CCACAGGGACTGTAGCCAGGCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGT 3153

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Qy       3154 GGCTGGGAGGCAGCTCT 3170

Db       2221 GGCTGGGAGGCAGCTCT 2237
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RESULT 3
BD063790

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LOCUS       BD063790               3599 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Insulin-like growth factor I(IGF)-1 expression system and methods
            of use.
ACCESSION   BD063790
VERSION     BD063790.1  GI:22609393
KEYWORDS    JP 2001505435-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 3599)
  AUTHORS   Coleman,M., Schwartz,R. and Demayo,F.J.
  TITLE     Insulin-like growth factor I(IGF)-1 expression system and methods
            of
  JOURNAL   Patent: JP 2001505435-A 3 24-APR-2001;
            BARENTIS INC,BAYLOR COLLEGE OF MEDICINE
COMMENT     PN   JP 2001505435-A/3
            PD   24-APR-2001
            PF   01-DEC-1997 JP 1998525696
            PR   02-DEC-1996 US    60/031539,19-NOV-1997 US    08/974572 PI
            MICHAEL COLEMAN,ROBERT SCHWARTZ,FRANCESCO J DEMAYO PC
            C12N15/85,C07K14/65,A61K48/00,A01K67/027
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
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ORIGIN
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Query Match 40.9%; Score 2218; DB 6; Length 3599;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2224; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249

Db          3 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 62

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309

Db         63 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 122

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369

Db        123 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 182

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
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Db        183 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 242
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Db        243 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 302
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Db        303 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 362
Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
Db        363 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 422
Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
Db        423 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 482
Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
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Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
Db        543 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 602
Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
Db        603 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 662
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Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
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Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
Db        783 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 842
Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
Db        843 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 902
Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
Db        903 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 962
Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
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Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
Db       1023 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 1082
Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
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Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
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Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
Db       1323 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 1382
Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
Db       1383 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 1442
Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
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Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
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Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
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Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
Db       1623 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 1682
Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
Db       1683 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 1742
Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
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Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
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Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
Db       1923 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 1982
Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
Db       1983 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 2042
Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
Db       2043 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 2102
Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
Db       2103 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 2162
Qy       5350 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 5409
Db       2163 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 2222
Qy       5410 GGCGAATTGGAGCT 5423
Db       2223 GGCGAATTGGAGCT 2236
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RESULT 4
BD069041
LOCUS BD069041 3599 bp DNA linear PAT 27-AUG-2002
DEFINITION Treatment for urinary incontinence using gene therapy techniques.
ACCESSION BD069041
VERSION BD069041.1 GI:22614644

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KEYWORDS    JP 2001511154-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3599)
  AUTHORS   Coleman,M.
  TITLE     Treatment for urinary incontinence using gene therapy techniques
  JOURNAL   Patent: JP 2001511154-A 3 07-AUG-2001;
            BARENTIS INC
COMMENT     OS   Unidentified
            PN   JP 2001511154-A/3
            PD   07-AUG-2001
            PF   04-FEB-1998 JP 1998533206
            PR   04-FEB-1997 US    60/036862
            PI   MICHAEL COLEMAN
            PC   A61K48/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Treatment for urinary incontinence using gene therapy  CC
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            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             40.9%;  Score 2218;  DB 6;  Length 3599;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2224;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
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Db          3 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 62

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
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Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
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Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
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Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
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Db        303 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 362

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
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Db        363 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 422

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
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Db        423 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 482

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
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Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
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Db         663 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 722

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
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Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
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Db         903 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 962

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Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
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Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
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Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
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Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
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Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
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Db        1563 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 1622

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Db        1623 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 1682
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Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
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Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
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Db       1803 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 1862

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Db       2103 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 2162

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Db       2163 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 2222

Qy       5410 GGCGAATTGGAGCT 5423
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Db       2223 GGCGAATTGGAGCT 2236


RESULT 5
CQ877111
LOCUS       CQ877111               3803 bp    DNA     linear   PAT 04-OCT-2004
DEFINITION  Sequence 2 from Patent WO2004081040.
ACCESSION   CQ877111
VERSION     CQ877111.1  GI:53790387
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Rabinovsky,E.D. and Draghia-Akli,R.
  TITLE     Insulin-like growth factor (igf-i) plasmid-mediated supplementation
            for therapeutic applications
  JOURNAL   Patent: WO 2004081040-A 2 23-SEP-2004;
            Advisys, Inc. (US); BAYLOR COLLEGE OF MEDICINE (US)
FEATURES             Location/Qualifiers
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                     /note="Nucleic acid sequence for the pAV2002 plasmid."
ORIGIN

  Query Match             40.9%;  Score 2218;  DB 6;  Length 3803;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2224;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
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Db       1570 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1629

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Db       3790 GGCGAATTGGAGCT 3803
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RESULT 6
BD063789
LOCUS BD063789 3600 bp DNA linear PAT 27-AUG-2002
DEFINITION Insulin-like growth factor I(IGF)-1 expression system and methods of use.
ACCESSION BD063789
VERSION BD063789.1 GI:22609392
KEYWORDS JP 2001505435-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 3600)
AUTHORS Coleman,M., Schwartz,R. and Demayo,F.J.
TITLE Insulin-like growth factor I(IGF)-1 expression system and methods of
JOURNAL Patent: JP 2001505435-A 2 24-APR-2001;
BARENTIS INC,BAYLOR COLLEGE OF MEDICINE
COMMENT PN JP 2001505435-A/2
PD 24-APR-2001
PF 01-DEC-1997 JP 1998525696
PR 02-DEC-1996 US 60/031539,19-NOV-1997 US 08/974572 PI
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C12N15/85,C07K14/65,A61K48/00,A01K67/027
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CC Topology: Linear;
FH Key Location/Qualifiers.
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ORIGIN

Query Match 40.9%; Score 2215.8; DB 6; Length 3600;
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Matches 2217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION  Treatment for urinary incontinence using gene therapy techniques.
ACCESSION   BD069040
VERSION     BD069040.1  GI:22614643
KEYWORDS    JP 2001511154-A/2.
SOURCE      unidentified
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REFERENCE   1  (bases 1 to 3600)
  AUTHORS   Coleman,M.
  TITLE     Treatment for urinary incontinence using gene therapy techniques
  JOURNAL   Patent: JP 2001511154-A 2 07-AUG-2001;
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COMMENT     OS   Unidentified
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ORIGIN

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Qy       3265 CTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGC 3324
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Qy       3325 ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGC 3384
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Db        139 ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGC 198

Qy       3385 TCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA 3444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA 258

Qy       3445 CGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG 3504
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG 318

Qy       3505 CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG 3564
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Db        319 CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG 378

Qy       3565 TTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG 3624
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Qy       3625 GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC 3684
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Qy       3685 GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA 3744
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Qy       3745 TACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTT 3804
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Qy       3805 ACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC 3864
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Db        619 ACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC 678

Qy       3865 TGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC 3924
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Db        679 TGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC 738

Qy       3925 CCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA 3984
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Db        739 CCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA 798

Qy       3985 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT 4044
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Db        799 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT 858

Qy       4045 GTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA 4104
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Db        859 GTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACA 918

Qy       4105 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT 4164
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Db        919 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT 978

Qy       4165 TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATT 4224
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Db        1099 CAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATA 1158

Qy       4345 CCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGG 4404
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Db        1159 CCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGG 1218

Qy       4405 GTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAAT 4464
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Db        1219 GTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAAT 1278

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Qy       4645 CGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGC 4704
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Qy       4705 GTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGA 4764
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Qy       4825 GTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGC 4884
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Qy       4885 GCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACC 4944
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Db        1699 GCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACC 1758

Qy       4945 GGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGT 5004
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Db        1759 GGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGT 1818

Qy       5005 GCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCA 5064
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Db        1819 GCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCA 1878

Qy       5065 TCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTG 5124
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Db        1879 TCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTG 1938

Qy       5125 CGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACC 5184
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Db        1939 CGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACC 1998

Qy       5185 TTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAG 5244
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Qy       5245 TCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCG 5304
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Db       2059 TCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCG 2118

Qy       5305 AAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGA 5364
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Db       2119 AAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGA 2178

Qy       5365 CGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGAGCT 5423
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Db       2179 CGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGAGCT 2237


RESULT 8
CQ854738
LOCUS       CQ854738               3558 bp    DNA     linear   PAT 23-AUG-2004
DEFINITION  Sequence 26 from Patent WO2004067719.
ACCESSION   CQ854738
VERSION     CQ854738.1  GI:51510298
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brown,P.A., Draghia-Akli,R. and Carpenter,R.H.
  TITLE     Reducing culling in herd animals growth hormone releasing
            hormone(ghrh)
  JOURNAL   Patent: WO 2004067719-A 26 12-AUG-2004;
            Advisys, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             40.8%;  Score 2211.6;  DB 6;  Length 3558;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 2217;  Conservative    1;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
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Db       1200 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1259

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1260 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1319

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1379

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
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Db       1380 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1439

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1440 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1499

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Db       1500 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1559

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
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Db       1560 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1619

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Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
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Db       1740 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1799

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
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Db       1800 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 1859

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
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Db       1860 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 1919

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
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Db       1920 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 1979

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
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Db       2040 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2099

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
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Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
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Db       2160 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2219

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
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Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
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Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
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Db       2520 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2579

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Db       2580 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2639

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Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
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Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
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Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
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Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
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Qy       5350 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 5409
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Qy       5410 GGCGAATT 5417
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CQ854723
LOCUS       CQ854723               3534 bp    DNA     linear   PAT 23-AUG-2004
DEFINITION  Sequence 11 from Patent WO2004067719.
ACCESSION   CQ854723
VERSION     CQ854723.1  GI:51510283
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brown,P.A., Draghia-Akli,R. and Carpenter,R.H.
  TITLE     Reducing culling in herd animals growth hormone releasing
            hormone(ghrh)
  JOURNAL   Patent: WO 2004067719-A 11 12-AUG-2004;
            Advisys, Inc. (US)
FEATURES             Location/Qualifiers
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                     /note="This is the nucleic acid sequence for the
                     operatively linked comp onents of the HV-GHRH plasmid."
ORIGIN
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Query Match 39.8%; Score 2160; DB 6; Length 3534;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
Db       1419 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1478

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
Db       1539 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1598

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
Db       1599 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1658

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
Db       1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
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Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
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Db       1959 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
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Db       2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318

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Db       2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378

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Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
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Db       2739 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2798

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
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Db       2799 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2858

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
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Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
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Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
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Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
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Db       3039 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3098

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
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Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
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Db       3159 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3218

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
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Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
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Db       3279 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3338

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
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Db       3339 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3398

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
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Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
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Db       3459 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3518

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RESULT 10
CQ854724
LOCUS       CQ854724               3534 bp    DNA     linear   PAT 23-AUG-2004
DEFINITION  Sequence 12 from Patent WO2004067719.
ACCESSION   CQ854724
VERSION     CQ854724.1  GI:51510284
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brown,P.A., Draghia-Akli,R. and Carpenter,R.H.
  TITLE     Reducing culling in herd animals growth hormone releasing
            hormone(ghrh)
  JOURNAL   Patent: WO 2004067719-A 12 12-AUG-2004;
            Advisys, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .3534
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
                     /note="Nucleic acid sequence for the TI-GHRH plasmid."
ORIGIN

  Query Match             39.8%;  Score 2160;  DB 6;  Length 3534;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 2166;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
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Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
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Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
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Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

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Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
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Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
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Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
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Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
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Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
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Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
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Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
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Db       2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
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Db       2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
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Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
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Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
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Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
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Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
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Db       3519 TTTTCCCAGTCACGAC 3534
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RESULT 11
CQ854725
LOCUS CQ854725 3534 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 13 from Patent WO2004067719.
ACCESSION CQ854725
VERSION CQ854725.1 GI:51510285
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brown,P.A., Draghia-Akli,R. and Carpenter,R.H.
TITLE Reducing culling in herd animals growth hormone releasing hormone(ghrh)
JOURNAL Patent: WO 2004067719-A 13 12-AUG-2004;
Advisys, Inc. (US)
FEATURES Location/Qualifiers
source 1. .3534
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Nucleic acid sequence for the TV-GHRH plasmid."
ORIGIN

Query Match 39.8%; Score 2160; DB 6; Length 3534;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
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Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
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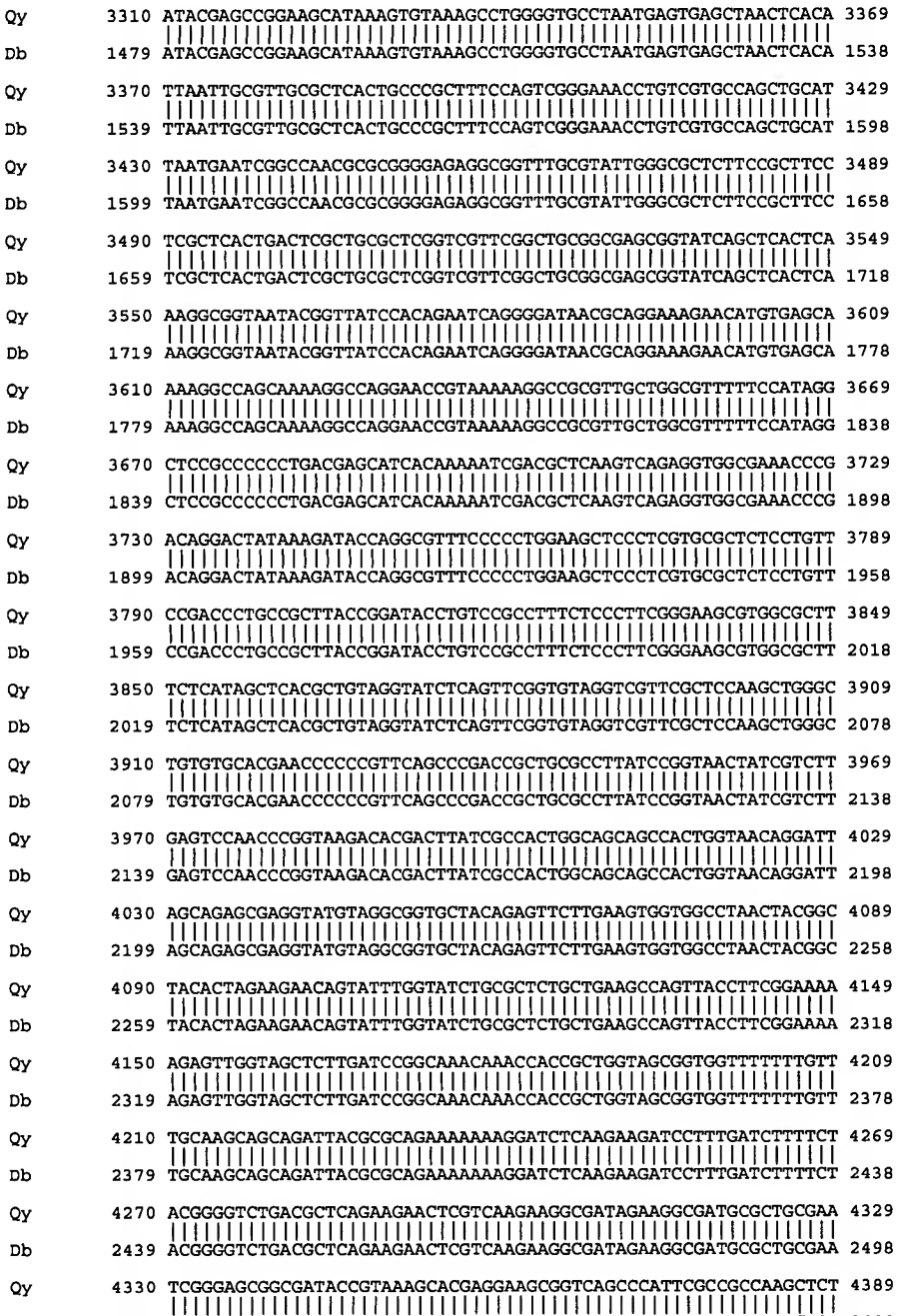

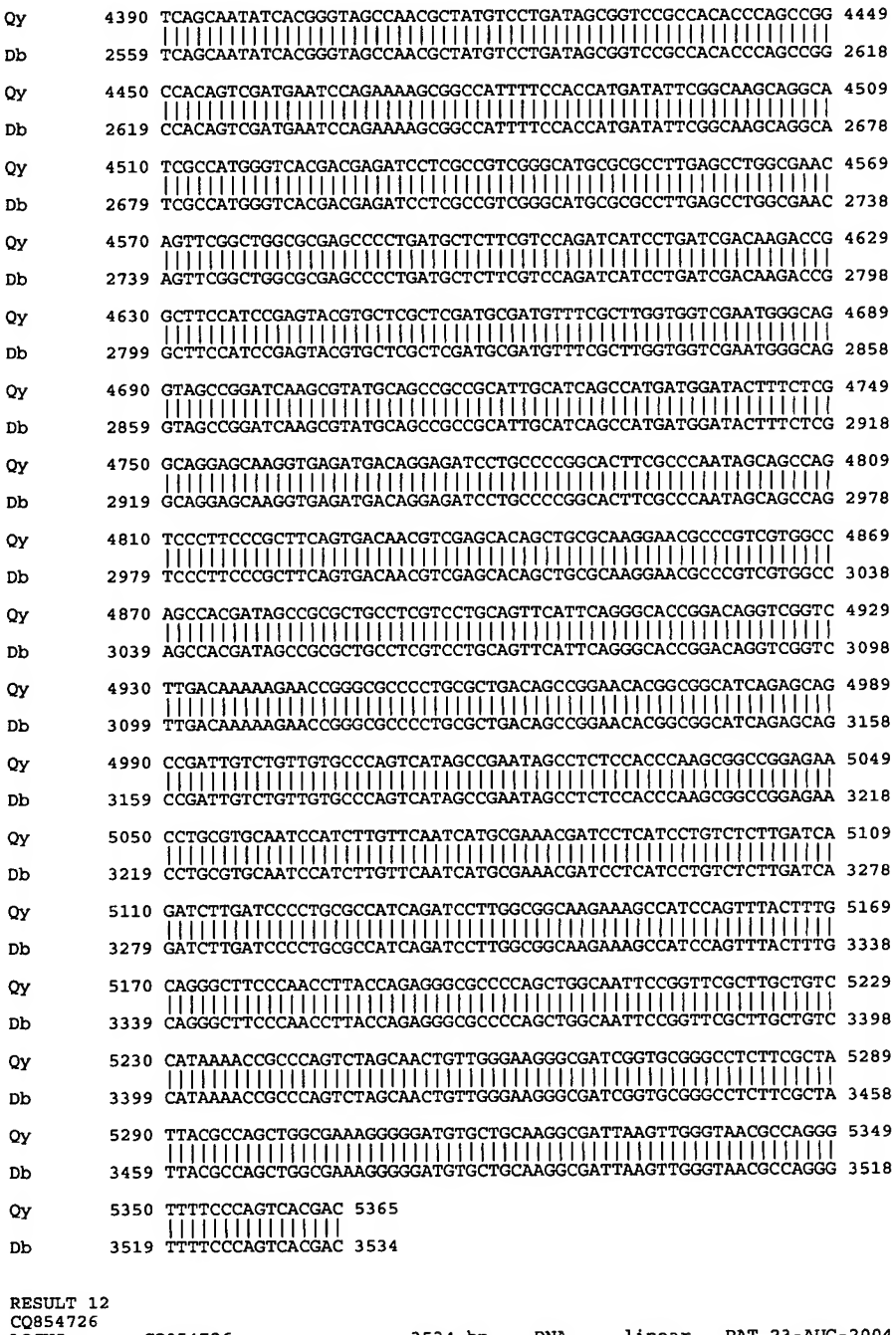

RESULT 12
CQ854726
LOCUS CQ854726 3534 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 14 from Patent WO2004067719.

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ACCESSION   CQ854726
VERSION     CQ854726.1  GI:51510286
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brown,P.A., Draghia-Akli,R. and Carpenter,R.H.
  TITLE     Reducing culling in herd animals growth hormone releasing
            hormone(ghrh)
  JOURNAL   Patent: WO 2004067719-A 14 12-AUG-2004;
            Advisys, Inc. (US)
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ORIGIN
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Query Match 39.8%; Score 2160; DB 6; Length 3534;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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RESULT 13
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DEFINITION  Sequence 15 from Patent WO2004067719.
ACCESSION   CQ854727
VERSION     CQ854727.1  GI:51510287
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brown,P.A., Draghia-Akli,R. and Carpenter,R.H.
  TITLE     Reducing culling in herd animals growth hormone releasing
            hormone(ghrh)
  JOURNAL   Patent: WO 2004067719-A 15 12-AUG-2004;
            Advisys, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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RESULT 14
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DEFINITION  Sequence 29 from Patent WO2004067719.
ACCESSION   CQ854741
VERSION     CQ854741.1  GI:51510301
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brown,P.A., Draghia-Akli,R. and Carpenter,R.H.
  TITLE     Reducing culling in herd animals growth hormone releasing
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  JOURNAL   Patent: WO 2004067719-A 29 12-AUG-2004;
            Advisys, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             39.8%;  Score 2160;  DB 6;  Length 3534;
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Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
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Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
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RESULT 15
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DEFINITION Sequence 11 from Patent WO2004093920.
ACCESSION CQ903781
VERSION CQ903781.1 GI:55785225
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Draghia-Akli,R., Scott,C. and Brown,P.A.
TITLE Plasmid mediated ghrh supplementation for renal failures
JOURNAL Patent: WO 2004093920-A 11 04-NOV-2004;
Advisys, Inc. (US)
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ORIGIN

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Qy      3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
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Qy      4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
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Qy      4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
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Qy      4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
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Qy      5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
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Perfect score: 5423
Sequence: 1 ccaccgcggtggcggccgtc.....ctatagggcgaattggagct 5423

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5423	100.0	5423	13	ADS73973	Ads73973 Plasmid p
2	4958.2	91.4	5707	2	AAX88055	Aax88055 Plasmid p
3	2785.8	51.4	6345	2	AAX88054	Aax88054 Plasmid p
4	2237	41.3	2237	13	ADS73977	Ads73977 Skeletal
5	2218	40.9	3599	2	AAV50428	Aav50428 Plasmid p
6	2218	40.9	3599	2	AAV40796	Aav40796 Actual se
7	2218	40.9	3803	13	ADS73974	Ads73974 Plasmid p
8	2215.8	40.9	3600	2	AAV50427	Aav50427 Plasmid p
9	2215.8	40.9	3600	2	AAV40795	Aav40795 Expected
10	2211.6	40.8	3558	9	AAL60457	Aal60457 pGR1774 p
11	2211.6	40.8	3558	13	ADR23406	Adr23406 Inducible
12	2160	39.8	2192	6	ABQ78294	Abq78294 Nucleotid
13	2160	39.8	3534	6	ABQ78293	Abq78293 Nucleotid
14	2160	39.8	3534	9	AAL62060	Aal62060 TV-GHRH p
15	2160	39.8	3534	9	AAL62062	Aal62062 Wild-type
16	2160	39.8	3534	9	AAL62059	Aal62059 TI-GHRH p
17	2160	39.8	3534	9	AAL62058	Aal62058 pSP-HV-GH
18	2160	39.8	3534	9	AAL62061	Aal62061 15/27/28-
19	2160	39.8	3534	9	AAL60444	Aal60444 TI-GHRH p
20	2160	39.8	3534	9	AAL60445	Aal60445 TV-GHRH p
21	2160	39.8	3534	9	AAL60446	Aal60446 15/27/28
22	2160	39.8	3534	9	AAL60443	Aal60443 pSP-HV-GH
23	2160	39.8	3534	9	AAL60447	Aal60447 Wild-type
24	2160	39.8	3534	10	ACF04661	Acf04661 Wildtype
25	2160	39.8	3534	10	ACF04660	Acf04660 15/27/28
26	2160	39.8	3534	10	ACF04657	Acf04657 HV-GHRH o
27	2160	39.8	3534	10	ACF04659	Acf04659 TV-GHRH o
28	2160	39.8	3534	10	ACF04658	Acf04658 TI-GHRH o
29	2160	39.8	3534	12	ADF90306	Adf90306 Wild type
30	2160	39.8	3534	12	ADF90302	Adf90302 HV-GHRH p
31	2160	39.8	3534	12	ADF90304	Adf90304 TV-GHRH p
32	2160	39.8	3534	12	ADF90305	Adf90305 15/27/28
33	2160	39.8	3534	12	ADF90303	Adf90303 TI-GHRH p
34	2160	39.8	3534	12	ADL70452	Adl70452 Protease
35	2160	39.8	3534	12	ADL70453	Adl70453 Protease
36	2160	39.8	3534	12	ADL70454	Adl70454 Protease
37	2160	39.8	3534	12	ADO31099	Ado31099 Cardiac s
38	2160	39.8	3534	12	ADO31100	Ado31100 Cardiac s
39	2160	39.8	3534	12	ADO31098	Ado31098 Cardiac s
40	2160	39.8	3534	12	ADO31101	Ado31101 Cardiac s
41	2160	39.8	3534	13	ADR23409	Adr23409 Codon opt
42	2160	39.8	3534	13	ADR23393	Adr23393 TI-GHRH p
43	2160	39.8	3534	13	ADR23394	Adr23394 TV-GHRH p
44	2160	39.8	3534	13	ADR23395	Adr23395 15/27/28-
45	2160	39.8	3534	13	ADR23392	Adr23392 Plasmid p

ALIGNMENTS

RESULT 1
ADS73973
ID ADS73973 standard; DNA; 5423 BP.
XX
AC ADS73973;
XX
DT 16-DEC-2004 (first entry)
XX
DE Plasmid pAV2001 nucleotide sequence.
XX
KW IGF-I; insulin-like growth factor I; myogenic promoter; MEF-1; MEF-2;
KW TEF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis;
KW vascular endothelial growth factor; VEGF; VEGF receptor; antidiabetic;
KW cardiant; vasotropic; ophthalmological; cerebroprotective; ds.
XX
OS Synthetic.
XX
PN WO2004081040-A2.
XX
PD 23-SEP-2004.
XX
PF 11-MAR-2004; 2004WO-US007295.
XX
PR 12-MAR-2003; 2003US-0454079P.
XX
PA (ADVI-) ADVISYS INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Rabinovsky ED, Draghia-Akli R;
XX
DR WPI; 2004-668935/65.
XX
PT New isolated nucleic acid expression construct having a myogenic
PT promoter, a nucleic acid sequence encoding IGF-Ile, and a 3'UTR, useful
PT for treating diabetes, ischemic heart and cerebrovascular disease.
XX
PS Claim 11; SEQ ID NO 1; 104pp; English.
XX
CC The invention relates to an isolated nucleic acid expression construct
CC comprising a myogenic promoter, a nucleic acid sequence encoding an
CC insulin-like growth factor I (IGF-I) or its functional biological
CC equivalent, and a 3' untranslated region (3'UTR), which has in vivo

CC expression activity for the encoded IGF-I in a tissue. The myogenic
CC promoter in the isolated nucleic acid expression construct comprises a
CC transcriptional loci from a family of MEF-1, MEF-2, TEF-1, SRE or SP. The
CC 3'UTR is from a skeletal alpha actin gene or from a human growth hormone.
CC The expression construct further comprises transfection-facilitating
CC vector system that is a plasmid, a viral vector, a liposome, or a
CC cationic lipid. The isolated nucleic acid expression construct also
CC comprises a transfection-facilitating polypeptide having a charged
CC polypeptide and/or poly-L-glutamate. The construct is useful in a method
CC for stimulating angiogenesis, or stimulating myogenesis, or elevating
CC levels of an angiogenic factor, or stimulating endogenous production of
CC an angiopoietin, or treating a muscular or vascular complications of
CC diabetes in a subject. The angiogenic factor comprises a vascular
CC endothelial growth factor (VEGF) or VEGF receptor. The methods and
CC compositions of the present invention are useful for the prevention
CC and/or treatment of diseases or conditions associated with aberrant
CC expression or activity of the IGF-I, such as diabetes mellitus, ischaemic
CC heart disease, diabetic retinopathy and cerebrovascular disease. The
CC present sequence represents the nucleotide sequence of a plasmid pAV2001,
CC a specific example of the isolated nucleic acid expression construct of
CC the invention.
XX
SQ Sequence 5423 BP; 1219 A; 1475 C; 1474 G; 1255 T; 0 U; 0 Other;

Query Match 100.0%; Score 5423; DB 13; Length 5423;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCACCGCGGTGGCGGCCGTCCGCCCTCGGCACCATCCTCACGACACCCAAATATGGCGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCACCGCGGTGGCGGCCGTCCGCCCTCGGCACCATCCTCACGACACCCAAATATGGCGAC 60

Qy         61 GGGTGAGGAATGGTGGGGAGTTATTTTTAGAGCGGTGAGGAAGGTGGGCAGGCAGCAGGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGTGAGGAATGGTGGGGAGTTATTTTTAGAGCGGTGAGGAAGGTGGGCAGGCAGCAGGT 120

Qy        121 GTTGGCGCTCTAAAAATAACTCCCGGGAGTTATTTTTAGAGCGGAGGAATGGTGGACACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTGGCGCTCTAAAAATAACTCCCGGGAGTTATTTTTAGAGCGGAGGAATGGTGGACACC 180

Qy        181 CAAATATGGCGACGGTTCCTCACCCGTCGCCATATTTGGGTGTCCGCCCTCGGCCGGGGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAAATATGGCGACGGTTCCTCACCCGTCGCCATATTTGGGTGTCCGCCCTCGGCCGGGGC 240

Qy        241 CGCATTCCTGGGGGCCGGGCGGTGCTCCCGCCCGCCTCGATAAAAGGCTCCGGGGCCGGC 300
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Db        241 CGCATTCCTGGGGGCCGGGCGGTGCTCCCGCCCGCCTCGATAAAAGGCTCCGGGGCCGGC 300

Qy        301 GGCGGCCCACGAGCTACCCGGAGGAGCGGGAGGCGCCAAGCTCTAGAACTAGTGGATCCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCGGCCCACGAGCTACCCGGAGGAGCGGGAGGCGCCAAGCTCTAGAACTAGTGGATCCC 360

Qy        361 AAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCCATGGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCCATGGGA 420

Qy        421 AAAATCAGCAGTCTTCCAACCCAATTATTTAAGTGCTGCTTTTGTGATTTCTTGAAGGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAAATCAGCAGTCTTCCAACCCAATTATTTAAGTGCTGCTTTTGTGATTTCTTGAAGGTG 480

Qy        481 AAGATGCACACCATGTCCTCCTCGCATCTCTTCTACCTGGCGCTGTGCCTGCTCACCTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAGATGCACACCATGTCCTCCTCGCATCTCTTCTACCTGGCGCTGTGCCTGCTCACCTTC 540

Qy        541 ACCAGCTCTGCCACGGCTGGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCAGCTCTGCCACGGCTGGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTT 600

Qy        601 CAGTTCGTGTGTGGAGACAGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGTTCGTGTGTGGAGACAGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGC 660

Qy        661 AGTCGGAGGGCGCCTCAGACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTCGGAGGGCGCCTCAGACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTA 720

Qy        721 AGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGT 780

Qy        781 GCCCAGCGCCACACCGACATGCCCAAGACCCAGAAGGAAGTACATTTGAAGAACGCAAGT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCCAGCGCCACACCGACATGCCCAAGACCCAGAAGGAAGTACATTTGAAGAACGCAAGT 840

Qy        841 AGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGA 900

Qy        901 GTGACATGCCACCGCAGGATCCCCCGGGCTGCAGGAATTCGATGGCCCATCCATTGTCCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGACATGCCACCGCAGGATCCCCCGGGCTGCAGGAATTCGATGGCCCATCCATTGTCCA 960

Qy        961 CCGTAAATGCTTCTAAACATGTTTACATGATCACTTTGCCAACCACACTCAGGATGACAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCGTAAATGCTTCTAAACATGTTTACATGATCACTTTGCCAACCACACTCAGGATGACAA 1020

Qy       1021 TCTTGTAGGTTCCAGGCTGCTGAGGACCTCCACCAGCCATGCAACTTTCTATTTTGTAAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCTTGTAGGTTCCAGGCTGCTGAGGACCTCCACCAGCCATGCAACTTTCTATTTTGTAAC 1080

Qy       1081 AATTTCTGGTTACTGTTGCTGCAAAGCTCCATGTGACACAGTGTATGTAAAGTGTACATA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AATTTCTGGTTACTGTTGCTGCAAAGCTCCATGTGACACAGTGTATGTAAAGTGTACATA 1140

Qy       1141 AATTAATTTATTTTACCTCGTTTTGTTTGTTTTTAAAACCAATGCCCTGTGGAAGGAAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AATTAATTTATTTTACCTCGTTTTGTTTGTTTTTAAAACCAATGCCCTGTGGAAGGAAAC 1200

Qy       1201 ATAAAACTTCAAGAAGCATTAAATCATCAGTCATTCTGTCACACCCCTAATGCAGTTGTT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ATAAAACTTCAAGAAGCATTAAATCATCAGTCATTCTGTCACACCCCTAATGCAGTTGTT 1260

Qy       1261 TCTGTCATCATTTCCCTGGGCTCTTCCATCTCTCGCTGACCTGGGACTGGGTGCTGGGGC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTGTCATCATTTCCCTGGGCTCTTCCATCTCTCGCTGACCTGGGACTGGGTGCTGGGGC 1320

Qy       1321 TGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGATGGCATGGGGAGAGTGATGGGATACTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGATGGCATGGGGAGAGTGATGGGATACTG 1380

Qy       1381 CTGGGGGGGGGGGACTCACCCTGCTGTGGGCTGCAGGAAGCCCATTGGTGCAGAGAGCAG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTGGGGGGGGGGGACTCACCCTGCTGTGGGCTGCAGGAAGCCCATTGGTGCAGAGAGCAG 1440

Qy       1441 CCTGGGATGCCCATGACACGGGCACCCACTGCACCGTGTTTCTCCCATGCCCAGTAGGGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCTGGGATGCCCATGACACGGGCACCCACTGCACCGTGTTTCTCCCATGCCCAGTAGGGA 1500

Qy       1501 AAGGGTTACGAGCGCCGTTCATTCTCAGCTTGTGAAGGATTTTGTTGGGCTCAGCCTGCC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGGGTTACGAGCGCCGTTCATTCTCAGCTTGTGAAGGATTTTGTTGGGCTCAGCCTGCC 1560

Qy       1561 AGAGCAGTAGCCAGGCATGCCTGTGCAGCTCCGAGCTGTGATGGACAGAGGCAAGGCTGC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGAGCAGTAGCCAGGCATGCCTGTGCAGCTCCGAGCTGTGATGGACAGAGGCAAGGCTGC 1620

Qy       1621 AGCTGAGGCCAGGTGGTGGGCACAGGTTAAATTAAGAGCTTTCCACTCCACTTATGGAAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1681 GCCCTCCTGCACTCACCCTGTCCCTGGGGCTGGGGGCAGCCAGGGCCACTTCCTCACCCC 1740
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Db       1681 GCCCTCCTGCACTCACCCTGTCCCTGGGGCTGGGGGCAGCCAGGGCCACTTCCTCACCCC 1740

Qy       1741 ACCTGACACACAAGGCTTTGCCTGCACAGCCAGGACCTCCTGTGGCCACAGACTCTTATA 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1741 ACCTGACACACAAGGCTTTGCCTGCACAGCCAGGACCTCCTGTGGCCACAGACTCTTATA 1800
Qy       1801 GATTCGCTGTGCCCTAGGAGACCAGGGGGCTTTCCCTGCCTGGCCTTCTGGCCCCGGCGA 1860
Db       1801 GATTCGCTGTGCCCTAGGAGACCAGGGGGCTTTCCCTGCCTGGCCTTCTGGCCCCGGCGA 1860
Qy       1861 CACTGCAGGAGCTGCCCTATCTGCCTCCTCTTAGATGGTCCTGGCAGGAAGGCTGCACTT 1920
Db       1861 CACTGCAGGAGCTGCCCTATCTGCCTCCTCTTAGATGGTCCTGGCAGGAAGGCTGCACTT 1920
Qy       1921 GGCTTGGGGCTGATCCATATTACCACTGCAGTAGGGACAGCACTGCTGGAAGAAAAGATG 1980
Db       1921 GGCTTGGGGCTGATCCATATTACCACTGCAGTAGGGACAGCACTGCTGGAAGAAAAGATG 1980
Qy       1981 ATTTTCAACTGAACTTACTATCCAGGCAGGTTATTGCTTTATTGTGATGGTGCTAAGAGT 2040
Db       1981 ATTTTCAACTGAACTTACTATCCAGGCAGGTTATTGCTTTATTGTGATGGTGCTAAGAGT 2040
Qy       2041 GCGTTCTTTCTCACTGTAATGATTTTGCCCTCATGTGTGAATACACTTTCCAATAACAGC 2100
Db       2041 GCGTTCTTTCTCACTGTAATGATTTTGCCCTCATGTGTGAATACACTTTCCAATAACAGC 2100
Qy       2101 ACAGCCTCCAAAGGGAATTTCTGCAGGAAGAGACAGTACCTGGTGTGGGAAGTCCCTGTG 2160
Db       2101 ACAGCCTCCAAAGGGAATTTCTGCAGGAAGAGACAGTACCTGGTGTGGGAAGTCCCTGTG 2160
Qy       2161 CAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGAGCAGGATCACATCCT 2220
Db       2161 CAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGAGCAGGATCACATCCT 2220
Qy       2221 TTCTTAAAAAGACAAACAGAAGGTAGTGTGTGACCTTGCTGTATTTACTATTTACGCGTT 2280
Db       2221 TTCTTAAAAAGACAAACAGAAGGTAGTGTGTGACCTTGCTGTATTTACTATTTACGCGTT 2280
Qy       2281 GTTGTTCAGTGGCACATACCTCAACGGGGATATGGAGAGCTATTTCCCCAACCCTCGCTG 2340
Db       2281 GTTGTTCAGTGGCACATACCTCAACGGGGATATGGAGAGCTATTTCCCCAACCCTCGCTG 2340
Qy       2341 CTGGACCCTGATCTGGGGTTTTCCTGTAGCTTAAGCGGTGCCAACTGCTTAAGTGATTGT 2400
Db       2341 CTGGACCCTGATCTGGGGTTTTCCTGTAGCTTAAGCGGTGCCAACTGCTTAAGTGATTGT 2400
Qy       2401 AGAATCAGTAAGGCTGGAAAAGACCACAGATCATTAAGTCCAACTGTCAGCCCCATCCCC 2460
Db       2401 AGAATCAGTAAGGCTGGAAAAGACCACAGATCATTAAGTCCAACTGTCAGCCCCATCCCC 2460
Qy       2461 ACCGCGCCCACTGTCACTCAGTGCCACATCCACGCATTTCTTGAACATCTCCAGGGACAG 2520
Db       2461 ACCGCGCCCACTGTCACTCAGTGCCACATCCACGCATTTCTTGAACATCTCCAGGGACAG 2520
Qy       2521 TGACTCCACCCGTCACCAGCTGTGCTTCAGAGCAGGCAGGGTGACAGTCTCAGTGCCAGT 2580
Db       2521 TGACTCCACCCGTCACCAGCTGTGCTTCAGAGCAGGCAGGGTGACAGTCTCAGTGCCAGT 2580
Qy       2581 TGCATCCTGCTGAAGAGCTTAACAGTGCAGTTTAACAACGGACTGATTTGTTGATGTGGT 2640
Db       2581 TGCATCCTGCTGAAGAGCTTAACAGTGCAGTTTAACAACGGACTGATTTGTTGATGTGGT 2640
Qy       2641 TGCTGAATCAGTACGTTGAGATGTCACTAAACTTTTTGGAGATTAATTTCAGGATGGAAC 2700
Db       2641 TGCTGAATCAGTACGTTGAGATGTCACTAAACTTTTTGGAGATTAATTTCAGGATGGAAC 2700
Qy       2701 ACATTCTTAACCCTGAAACCAGCCTTTGATTTGGGCTTGGCATTTGCAGAATTTGCAGGA 2760
Db       2701 ACATTCTTAACCCTGAAACCAGCCTTTGATTTGGGCTTGGCATTTGCAGAATTTGCAGGA 2760
Qy       2761 AAAGATTGTTTGGGAACAGATGAATGGAATTTCCACCAAACAGAAAATTAACACTTACAC 2820
Db       2761 AAAGATTGTTTGGGAACAGATGAATGGAATTTCCACCAAACAGAAAATTAACACTTACAC 2820
Qy       2821 CAGTTTGAGTCTGGTCTTCGTTCGATATTTCTTAAGAATCTCATCATCCTCCCTGCTCTT 2880
Db       2821 CAGTTTGAGTCTGGTCTTCGTTCGATATTTCTTAAGAATCTCATCATCCTCCCTGCTCTT 2880
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Qy       2881 GGACCAGTGCTGCTGACAGGAGGTGGAGGATCATCAGGGTCAGCATCCTCAGCATCTAGG 2940
Db       2881 GGACCAGTGCTGCTGACAGGAGGTGGAGGATCATCAGGGTCAGCATCCTCAGCATCTAGG 2940
Qy       2941 GATGTGCACTATGTGTGATGGTGACACTTTAGAGAACTGCTTTGATTCCCCAGGGCTTTC 3000
Db       2941 GATGTGCACTATGTGTGATGGTGACACTTTAGAGAACTGCTTTGATTCCCCAGGGCTTTC 3000
Qy       3001 CCTCTCTTCCATGCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAACTTCCAGC 3060
Db       3001 CCTCTCTTCCATGCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAACTTCCAGC 3060
Qy       3061 ACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAGGCATGACC 3120
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Qy       3121 TTTTCCCAGCCGTGCTCTGAATCCAGCACTGGTGGCTGGGAGGCAGCTCTGGTCCTGGGG 3180
Db       3121 TTTTCCCAGCCGTGCTCTGAATCCAGCACTGGTGGCTGGGAGGCAGCTCTGGTCCTGGGG 3180
Qy       3181 TGCTGCAGTGAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCG 3240
Db       3181 TGCTGCAGTGAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCG 3240
Qy       3241 AGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATT 3300
Db       3241 AGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATT 3300
Qy       3301 CCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGC 3360
Db       3301 CCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGC 3360
Qy       3361 TAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGC 3420
Db       3361 TAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGC 3420
Qy       3421 CAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCT 3480
Db       3421 CAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCT 3480
Qy       3481 TCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCA 3540
Db       3481 TCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCA 3540
Qy       3541 GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAAC 3600
Db       3541 GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAAC 3600
Qy       3601 ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT 3660
Db       3601 ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT 3660
Qy       3661 TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGG 3720
Db       3661 TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGG 3720
Qy       3721 CGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGC 3780
Db       3721 CGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGC 3780
Qy       3781 TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGC 3840
Db       3781 TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGC 3840
Qy       3841 GTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCC 3900
Db       3841 GTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCC 3900
Qy       3901 AAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAAC 3960
Db       3901 AAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAAC 3960
```

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Qy       3961 TATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 TATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT 4020

Qy       4021 AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT 4080

Qy       4081 AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC 4140

Qy       4141 TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGT 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGT 4200

Qy       4201 TTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 TTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG 4260

Qy       4261 ATCTTTTCTACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 ATCTTTTCTACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATG 4320

Qy       4321 CGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCG 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 CGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCG 4380

Qy       4381 CCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACA 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 CCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACA 4440

Qy       4441 CCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGC 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 CCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGC 4500

Qy       4501 AAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGC 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 AAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGC 4560

Qy       4561 CTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCG 4620

Qy       4621 ACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCG 4680
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Db       4621 ACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCG 4680

Qy       4681 AATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGAT 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 AATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGAT 4740

Qy       4741 ACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAAT 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 ACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAAT 4800

Qy       4801 AGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCC 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 AGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCC 4860

Qy       4861 GTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGAC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGAC 4920

Qy       4921 AGGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCA 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 AGGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCA 4980

Qy       4981 TCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCG 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 TCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCG 5040

Qy       5041 GCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 GCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTC 5100

Qy       5101 TCTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAG 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 TCTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAG 5160

Qy       5161 TTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCG 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 TTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCG 5220

Qy       5221 CTTGCTGTCCATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCC 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 CTTGCTGTCCATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCC 5280

Qy       5281 TCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTA 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5281 TCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTA 5340

Qy       5341 ACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGAC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5401 TCACTATAGGGCGAATTGGAGCT 5423
             |||||||||||||||||||||||
Db       5401 TCACTATAGGGCGAATTGGAGCT 5423
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RESULT 2
AAX88055
ID AAX88055 standard; DNA; 5707 BP.
XX
AC AAX88055;
XX
DT 08-SEP-1999 (first entry)
XX
DE Plasmid pIG0335 DNA.
XX
KW Plasmid pIG0335; expression vector; treatment; disease;
KW RNA stability element; gene therapy; muscle atrophy; neurological;
KW muscular disease; systemic disease; aging; trophic factor; haemophilia;
KW clotting factor; atherogenesis; atherosclerotic; cardiovascular;
KW cerebrovascular; peripheral-vascular disease; hormone deficiency;
KW diabetes; transgenic animal; carcinogen; regulatory element;
KW livestock improvement; immune response; ds.
XX
OS Synthetic.
XX
PN US5925564-A.
XX
PD 20-JUL-1999.
XX
PF 07-JUN-1995; 95US-00472809.
XX
PR 06-NOV-1991; 91US-00789919.
PR 09-MAR-1994; 94US-00209846.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI O'malley BW, Demayo FJ, Schwartz RJ;
XX
DR WPI; 1999-418276/35.
XX
PT New expression vector system useful for gene therapy.
XX
PS Disclosure; Fig 17-17F; 67pp; English.
XX
CC This invention describes novel expression vector systems containing RNA
CC stability elements from 3' flanking sequences used for establishing
CC expression of a nucleic acid sequence within a tissue. The vectors also
CC facilitate enhanced expression in tissues and target expression with
CC tissue specificity. The expression vectors can be used to treat diseases
CC through gene therapy by targeting the vector to specific tissues.

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CC   Diseases that can be treated include muscle atrophy associated with
CC   neurological, muscular or systemic disease, aging by causing tissues to
CC   express trophic factors, haemophilia by causing tissues to express and
CC   secrete clotting factor into the circulation, atherogenesis and
CC   atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular
CC   disease by causing tissues to express factors involved in tissue
CC   metabolism. They can be used to replace genes of inherited genetic
CC   defects or acquired hormone deficiencies e.g. diabetes. To transform
CC   cells to produce particular proteins or RNA in vitro. To create
CC   transgenic animals which can be used for research into human diseases,
CC   assessing novel therapeutic methods, assessing the effect of chemical and
CC   physical carcinogens and for studying the effect of genes and genetic
CC   regulatory elements or livestock improvement. They can be used to induce
CC   an immune response. These vectors provide controlled expression of the
CC   genes they carry and produce a significantly high level of expression.
CC   Using 3'UTR sequences reduces the decay rates of the mRNAs encoded by the
CC   vectors which causes increased expression
XX
SQ   Sequence 5707 BP; 1221 A; 1634 C; 1576 G; 1276 T; 0 U; 0 Other;

  Query Match           91.4%;  Score 4958.2;  DB 2;  Length 5707;
  Best Local Similarity  99.2%;  Pred. No. 0;
  Matches 5007;  Conservative    0;  Mismatches    4;  Indels   37;  Gaps    1;

Qy        413 CCATGGGAAAAATCAGCAGTCTTCCAACCCAATTATTTAAGTGCTGCTTTTGTGATTTCT 472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 CCATGGGAAAAATCAGCAGTCTTCCAACCCAATTATTTAAGTGCTGCTTTTGTGATTTCT 706

Qy        473 TGAAGGTGAAGATGCACACCATGTCCTCCTCGCATCTCTTCTACCTGGCGCTGTGCCTGC 532
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 TGAAGGTGAAGATGCACACCATGTCCTCCTCGCATCTCTTCTACCTGGCGCTGTGCCTGC 766

Qy        533 TCACCTTCACCAGCTCTGCCACGGCTGGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGG 592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 TCACCTTCACCAGCTCTGCCACGGCTGGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGG 826

Qy        593 ATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTCAACAAGCCCACAGGGTATG 652
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 ATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTCAACAAGCCCACAGGGTATG 886

Qy        653 GCTCCAGCAGTCGGAGGGCGCCTCAGACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCT 712
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        887 GCTCCAGCAGTCGGAGGGCGCCTCAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCT 946

Qy        713 GTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCT 772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        947 GTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCT 1006

Qy        773 CTGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACCCAGAAGGAAGTACATTTGAAGA 832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1007 CTGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACCCAGAAGGAAGTACATTTGAAGA 1066

Qy        833 ACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCCTCCTGAGG 892
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1067 ACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCCTCCTGAGG 1126

Qy        893 AGTGAAGAGTGACATGCCACCGCAGGATCCCCCGGGCTGCAGGAATTCGATGGCCCATCC 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1127 AGTGAAGAGTGACATGCCACCGCAGGATCCCCCGGGCTGCAGGAATTCGATGGCCCATCC 1186

Qy        953 ATTGTCCACCGTAAATGCTTCTAAACATGTTTACATGATCACTTTGCCAACCACACTCAG 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1187 ATTGTCCACCGTAAATGCTTCTAAACATGTTTACATGATCACTTTGCCAACCACACTCAG 1246

Qy       1013 GATGACAATCTTGTAGGTTCCAGGCTGCTGAGGACCTCCACCAGCCATGCAACTTTCTAT 1072
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1247 GATGACAATCTTGTAGGTTCCAGGCTGCTGAGGACCTGCACCAGCCATGCAACTTTCTAT 1306

Qy       1073 TTTGTAACAATTTCTGGTTACTGTTGCTGCAAAGCTCCATGTGACACAGTGTATGTAAAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1307 TTTGTAACAATTTCTGGTTACTGTTGCTGCAAAGCTCCATGTGACACAGTGTATGTAAAG 1366

Qy       1133 TGTACATAAATTAATTTATTTTACCTCGTTTTGTTTGTTTTTAAAACCAATGCCCTGTGG 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1367 TGTACATAAATTAATTTATTTTACCTCGTTTTGTTTGTTTTTAAAACCAATGCCCTGTGG 1426

Qy       1193 AAGGAAACATAAAACTTCAAGAAGCATTAAATCATCAGTCATTCTGTCACACCCCTAATG 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1427 AAGGAAACATAAAACTTCAAGAAGCATTAAATCATCAGTCATTCTGTCACACCCCTAATG 1486

Qy       1253 CAGTTGTTTCTGTCATCATTTCCCTGGGCTCTTCCATCTCTCGCTGACCTGGGACTGGGT 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1487 CAGTTGTTTCTGTCATCATTTCCCTGGGCTCTTCCATCTCTCGCTGACCTGGGACTGGGT 1546

Qy       1313 GCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGATGGCATGGGGAGAGTGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1547 GCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGATGGCATGGGGAGAGTGATG 1606

Qy       1373 GGATACTGCTGGGGGGGGGGGACTCACCCTGCTGTGGGCTGCAGGAAGCCCATTGGTGCA 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1607 GGATACTGCTGGGGGGGGGGGACTCACCCTGCTGTGGGCTGCAGGAAGCCCATTGGTGCA 1666

Qy       1433 GAGAGCAGCCTGGGATGCCCATGACACGGGCACCCACTGCACCGTGTTTCTCCCATGCCC 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1667 GAGAGCAGCCTGGGATGCCCATGACACGGGCACCCACTGCACCGTGTTTCTCCCATGCCC 1726

Qy       1493 AGTAGGGAAAGGGTTACGAGCGCCGTTCATTCTCAGCTTGTGAAGGATTTTGTTGGGCTC 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1727 AGTAGGGAAAGGGTTACGAGCGCCGTTCATTCTCAGCTTGTGAAGGATTTTGTTGGGCTC 1786

Qy       1553 AGCCTGCCAGAGCAGTAGCCAGGCATGCCTGTGCAGCTCCGAGCTGTGATGGACAGAGGC 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1787 AGCCTGCCAGAGCAGTAGCCAGGCATGCCTGTGCAGCTCCGAGCTGTGATGGACAGAGGC 1846

Qy       1613 AAGGCTGCAGCTGAGGCCAGGTGGTGGGCACAGGTTAAATTAAGAGCTTTCCACTCCACT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1847 AAGGCTGCAGCTGAGGCCAGGTGGTGGGCACAGGTTAAATTAAGAGCTTTCCACTCCACT 1906

Qy       1673 TATGGAAAGCCCTCCTGCACTCACCCTGTCCCTGGGGCTGGGGGCAGCCAGGGCCACTTC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1907 TATGGAAAGCCCTCCTGCACTCACCCTGTCCCTGGGGCTGGGGGCAGCCAGGGCCACTTC 1966

Qy       1733 CTCACCCCACCTGACACACAAGGCTTTGCCTGCACAGCCAGGACCTCCTGTGGCCACAGA 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1967 CTCACCCCACCTGACACACAAGGCTTTGCCTGCACAGCCAGGACCTCCTGTGGCCACAGA 2026

Qy       1793 CTCTTATAGATTCGCTGTGCCCTAGGAGACCAGGGGGCTTTCCCTGCCTGGCCTTCTGGC 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2027 CTCTTATAGATTCGCTGTGCCCTAGGAGACCAGGGGGCTTTCCCTGCCTGGCCTTCTGGC 2086

Qy       1853 CCCGGCGACACTGCAGGAGCTGCCCTATCTGCCTCCTCTTAGATGGTCCTGGCAGGAAGG 1912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2087 CCCGGCGACACTGCAGGAGCTGCCCTATCTGCCTCCTCTTAGATGGTCCTGGCAGGAAGG 2146

Qy       1913 CTGCACTTGGCTTGGGGCTGATCCATATTACCACTGCAGTAGGGACAGCACTGCTGGAAG 1972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2147 CTGCACTTGGCTTGGGGCTGATCCATATTACCACTGCAGTAGGGACAGCACTGCTGGAAG 2206

Qy       1973 AAAAGATGATTTTCAACTGAACTTACTATCCAGGCAGGTTATTGCTTTATTGTGATGGTG 2032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2207 AAAAGATGATTTTCAACTGAACTTACTATCCAGGCAGGTTATTGCTTTATTGTGATGGTG 2266

Qy       2033 CTAAGAGTGCGTTCTTTCTCACTGTAATGATTTTGCCCTCATGTGTGAATACACTTTCCA 2092
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Db       2267 CTAAGAGTGCGTTCTTTCTCACTGTAATGATTTTGCCCTCATGTGTGAATACACTTTCCA 2326

Qy       2093 ATAACAGCACAGCCTCCAAAGGGAATTTCTGCAGGAAGAGACAGTACCTGGTGTGGGAAG 2152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2327 ATAACAGCACAGCCTCCAAAGGGAATTTCTGCAGGAAGAGACAGTACCTGGTGTGGGAAG 2386

Qy       2153 TCCCTGTGCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGAGCAGGAT 2212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2387 TCCCTGTGCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGAGCAGGAT 2446

Qy       2213 CACATCCTTTCTTAAAAAGACAAACAGAAGGTAGTGTGTGACCTTGCTGTATTTACTATT 2272
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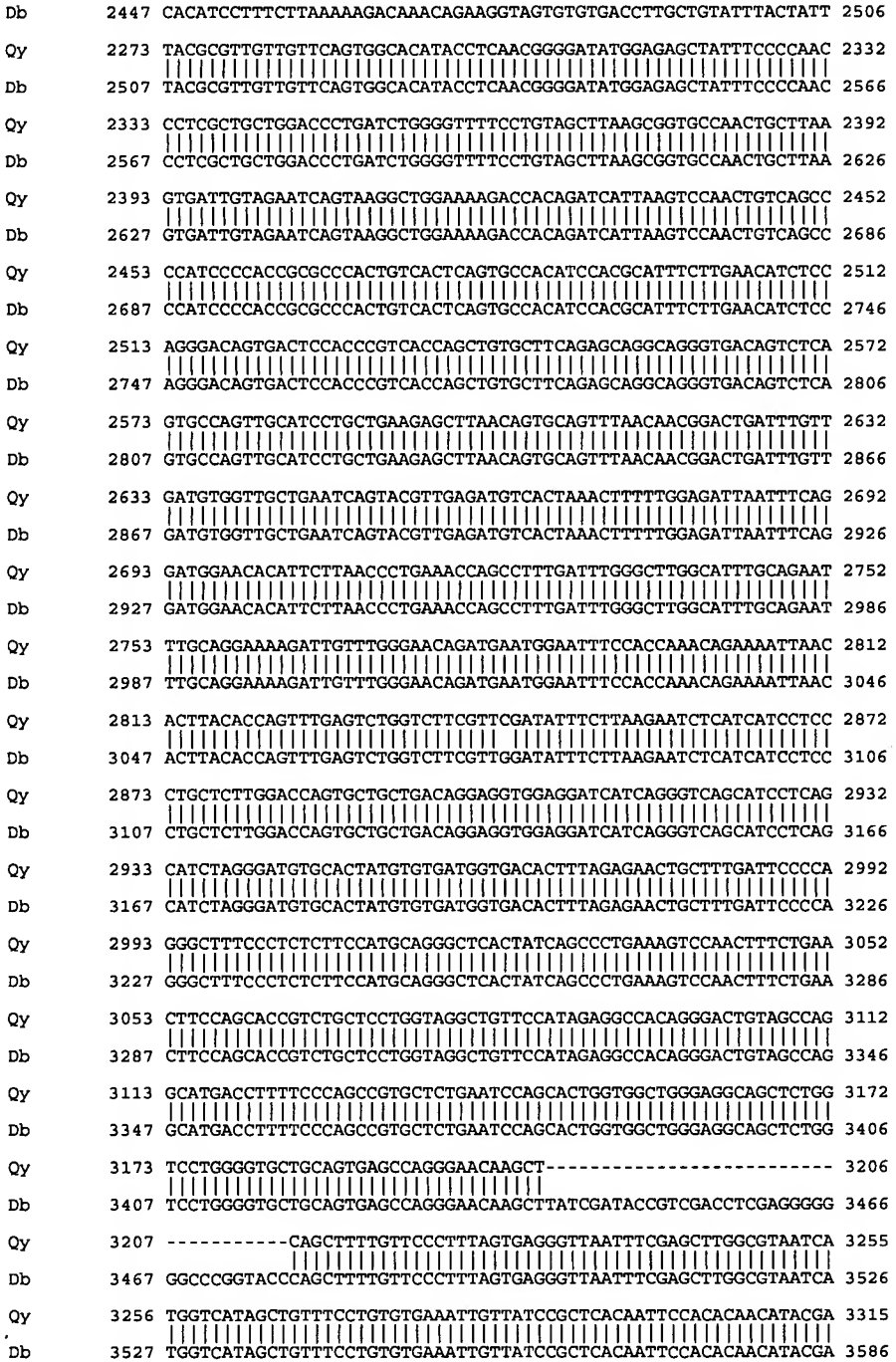
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Qy 2273 TACGCGTTGTTGTTCAGTGGCACATACCTCAACGGGGATATGGAGAGCTATTTCCCCAAC 2332
Db 2507 TACGCGTTGTTGTTCAGTGGCACATACCTCAACGGGGATATGGAGAGCTATTTCCCCAAC 2566
Qy 2333 CCTCGCTGCTGGACCCTGATCTGGGGTTTTCCTGTAGCTTAAGCGGTGCCAACTGCTTAA 2392
Db 2567 CCTCGCTGCTGGACCCTGATCTGGGGTTTTCCTGTAGCTTAAGCGGTGCCAACTGCTTAA 2626
Qy 2393 GTGATTGTAGAATCAGTAAGGCTGGAAAAGACCACAGATCATTAAGTCCAACTGTCAGCC 2452
Db 2627 GTGATTGTAGAATCAGTAAGGCTGGAAAAGACCACAGATCATTAAGTCCAACTGTCAGCC 2686
Qy 2453 CCATCCCCACCGCGCCCACTGTCACTCAGTGCCACATCCACGCATTTCTTGAACATCTCC 2512
Db 2687 CCATCCCCACCGCGCCCACTGTCACTCAGTGCCACATCCACGCATTTCTTGAACATCTCC 2746
Qy 2513 AGGGACAGTGACTCCACCCGTCACCAGCTGTGCTTCAGAGCAGGCAGGGTGACAGTCTCA 2572
Db 2747 AGGGACAGTGACTCCACCCGTCACCAGCTGTGCTTCAGAGCAGGCAGGGTGACAGTCTCA 2806
Qy 2573 GTGCCAGTTGCATCCTGCTGAAGAGCTTAACAGTGCAGTTTAACAACGGACTGATTTGTT 2632
Db 2807 GTGCCAGTTGCATCCTGCTGAAGAGCTTAACAGTGCAGTTTAACAACGGACTGATTTGTT 2866
Qy 2633 GATGTGGTTGCTGAATCAGTACGTTGAGATGTCACTAAACTTTTTGGAGATTAATTTCAG 2692
Db 2867 GATGTGGTTGCTGAATCAGTACGTTGAGATGTCACTAAACTTTTTGGAGATTAATTTCAG 2926
Qy 2693 GATGGAACACATTCTTAACCCTGAAACCAGCCTTTGATTTGGGCTTGGCATTTGCAGAAT 2752
Db 2927 GATGGAACACATTCTTAACCCTGAAACCAGCCTTTGATTTGGGCTTGGCATTTGCAGAAT 2986
Qy 2753 TTGCAGGAAAAGATTGTTTGGGAACAGATGAATGGAATTTCCACCAAACAGAAAATTAAC 2812
Db 2987 TTGCAGGAAAAGATTGTTTGGGAACAGATGAATGGAATTTCCACCAAACAGAAAATTAAC 3046
Qy 2813 ACTTACACCAGTTTGAGTCTGGTCTTCGTTCGATATTTCTTAAGAATCTCATCATCCTCC 2872
Db 3047 ACTTACACCAGTTTGAGTCTGGTCTTCGTTGGATATTTCTTAAGAATCTCATCATCCTCC 3106
Qy 2873 CTGCTCTTGGACCAGTGCTGCTGACAGGAGGTGGAGGATCATCAGGGTCAGCATCCTCAG 2932
Db 3107 CTGCTCTTGGACCAGTGCTGCTGACAGGAGGTGGAGGATCATCAGGGTCAGCATCCTCAG 3166
Qy 2933 CATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGAGAACTGCTTTGATTCCCCA 2992
Db 3167 CATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGAGAACTGCTTTGATTCCCCA 3226
Qy 2993 GGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA 3052
Db 3227 GGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA 3286
Qy 3053 CTTCCAGCACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAG 3112
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Qy 3113 GCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGTGGCTGGGAGGCAGCTCTGG 3172
Db 3347 GCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGTGGCTGGGAGGCAGCTCTGG 3406
Qy 3173 TCCTGGGGTGCTGCAGTGAGCCAGGGAACAAGCT---------- 3206
Db 3407 TCCTGGGGTGCTGCAGTGAGCCAGGGAACAAGCTTATCGATACCGTCGACCTCGAGGGGG 3466
Qy 3207 ----------CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCA 3255
Db 3467 GGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCA 3526
Qy 3256 TGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGA 3315
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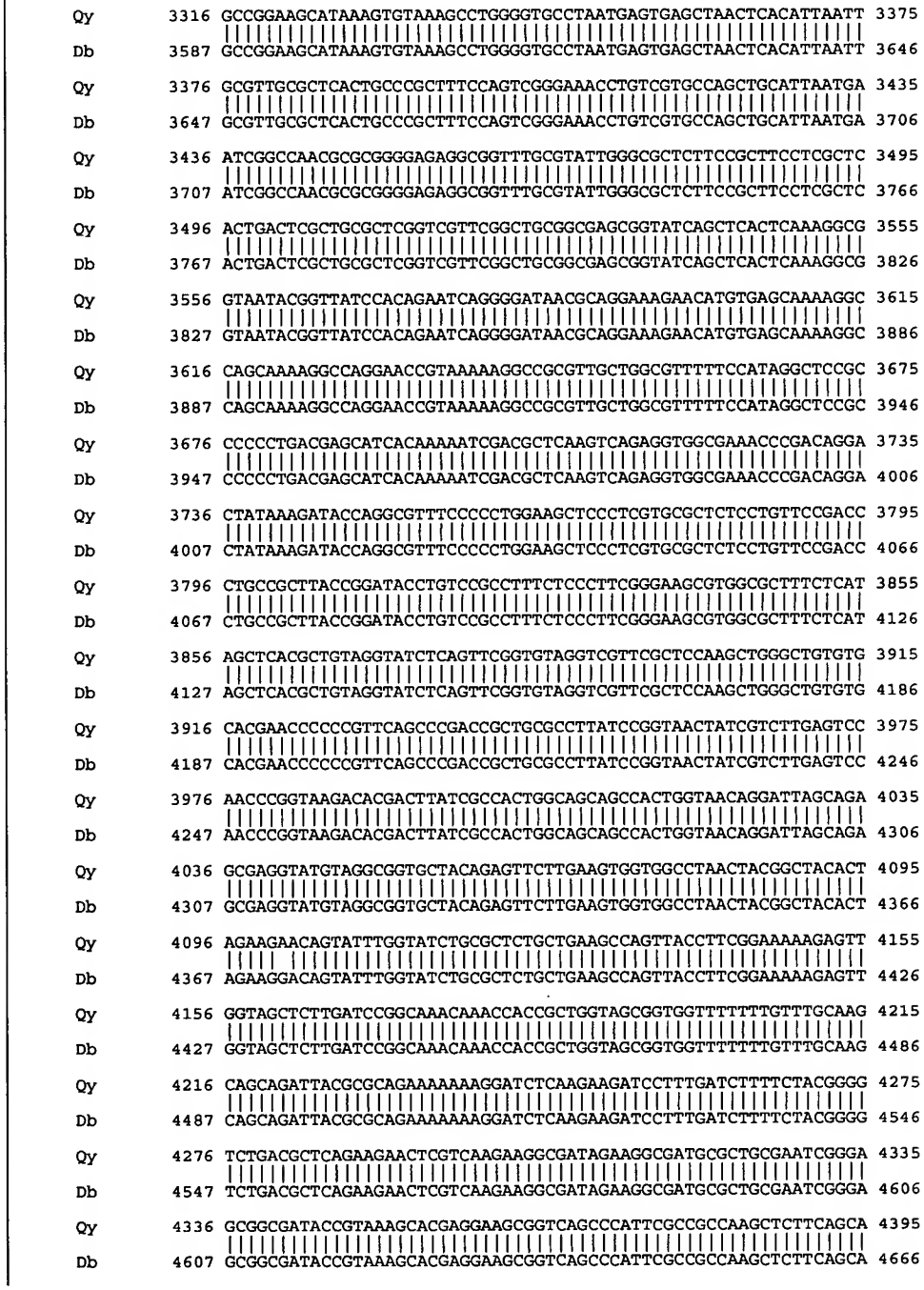
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Qy 3376 GCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGA 3435
Db 3647 GCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGA 3706
Qy 3436 ATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTC 3495
Db 3707 ATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTC 3766
Qy 3496 ACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCG 3555
Db 3767 ACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCG 3826
Qy 3556 GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGC 3615
Db 3827 GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGC 3886
Qy 3616 CAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC 3675
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Qy 3736 CTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC 3795
Db 4007 CTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC 4066
Qy 3796 CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAT 3855
Db 4067 CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAT 4126
Qy 3856 AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTG 3915
Db 4127 AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTG 4186
Qy 3916 CACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC 3975
Db 4187 CACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC 4246
Qy 3976 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA 4035
Db 4247 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA 4306
Qy 4036 GCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACT 4095
Db 4307 GCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACT 4366
Qy 4096 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTT 4155
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Qy 4156 GGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAG 4215
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Qy 4336 GCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCA 4395
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Qy       4396 ATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAG 4455
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Db       4667 ATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAG 4726

Qy       4456 TCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCA 4515
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4516 TGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCG 4575
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Qy       4576 GCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCC 4635
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Qy       4636 ATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCC 4695
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4907 ATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCC 4966

Qy       4696 GGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGA 4755
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Db       4967 GGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGA 5026

Qy       4756 GCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTT 4815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5027 GCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTT 5086

Qy       4816 CCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCAC 4875
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5087 CCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCAC 5146

Qy       4876 GATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACA 4935
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5147 GATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACA 5206

Qy       4936 AAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATT 4995
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Qy       4996 GTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCG 5055
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Db       5267 GTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCG 5326

Qy       5056 TGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTT 5115
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5327 TGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTT 5386

Qy       5116 GATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGC 5175
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5387 GATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGC 5446

Qy       5176 TTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAA 5235
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Qy       5236 ACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGC 5295
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Qy       5296 CAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCC 5355
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Qy       5356 CAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 5415
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Qy       5416 TTGGAGCT 5423
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Db       5687 TTGGAGCT 5694
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RESULT 3
AAX88054
ID AAX88054 standard; DNA; 6345 BP.
XX
AC AAX88054;
XX
DT 08-SEP-1999 (first entry)
XX
DE Plasmid pIG0100A DNA.
XX
KW Plasmid pIG0100A; plasmid pIG0335; expression vector; treatment; disease;
KW RNA stability element; gene therapy; muscle atrophy; neurological;
KW muscular disease; systemic disease; aging; trophic factor; haemophilia;
KW clotting factor; atherogenesis; atherosclerotic; cardiovascular;
KW cerebrovascular; peripheral-vascular disease; hormone deficiency;
KW diabetes; transgenic animal; carcinogen; regulatory element;
KW livestock improvement; immune response; ds.
XX
OS Synthetic.
XX
PN US5925564-A.
XX
PD 20-JUL-1999.
XX
PF 07-JUN-1995; 95US-00472809.
XX
PR 06-NOV-1991; 91US-00789919.
PR 09-MAR-1994; 94US-00209846.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI O'malley BW, Demayo FJ, Schwartz RJ;
XX
DR WPI; 1999-418276/35.
XX
PT New expression vector system useful for gene therapy.
XX
PS Disclosure; Fig 15-15G; 67pp; English.
XX
CC This invention describes novel expression vector systems containing RNA
CC stability elements from 3' flanking sequences used for establishing
CC expression of a nucleic acid sequence within a tissue. The vectors also
CC facilitate enhanced expression in tissues and target expression with
CC tissue specificity. The expression vectors can be used to treat diseases
CC through gene therapy by targeting the vector to specific tissues.
CC Diseases that can be treated include muscle atrophy associated with
CC neurological, muscular or systemic disease, aging by causing tissues to
CC express trophic factors, haemophilia by causing tissues to express and
CC secrete clotting factor into the circulation, atherogenesis and
CC atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular
CC disease by causing tissues to express factors involved in tissue
CC metabolism. They can be used to replace genes of inherited genetic
CC defects or acquired hormone deficiencies e.g. diabetes. To transform
CC cells to produce particular proteins or RNA in vitro. To create
CC transgenic animals which can be used for research into human diseases,
CC assessing novel therapeutic methods, assessing the effect of chemical and
CC physical carcinogens and for studying the effect of genes and genetic
CC regulatory elements or livestock improvement. They can be used to induce
CC an immune response. These vectors provide controlled expression of the
CC genes they carry and produce a significantly high level of expression.
CC Using 3'UTR sequences reduces the decay rates of the mRNAs encoded by the
CC vectors which causes increased expression
XX
SQ Sequence 6345 BP; 1453 A; 1702 C; 1689 G; 1501 T; 0 U; 0 Other;

Query Match 51.4%; Score 2785.8; DB 2; Length 6345;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2787; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        413 CCATGGGAAAAATCAGCAGTCTTCCAACCCAATTATTTAAGTGCTGCTTTTGTGATTTCT 472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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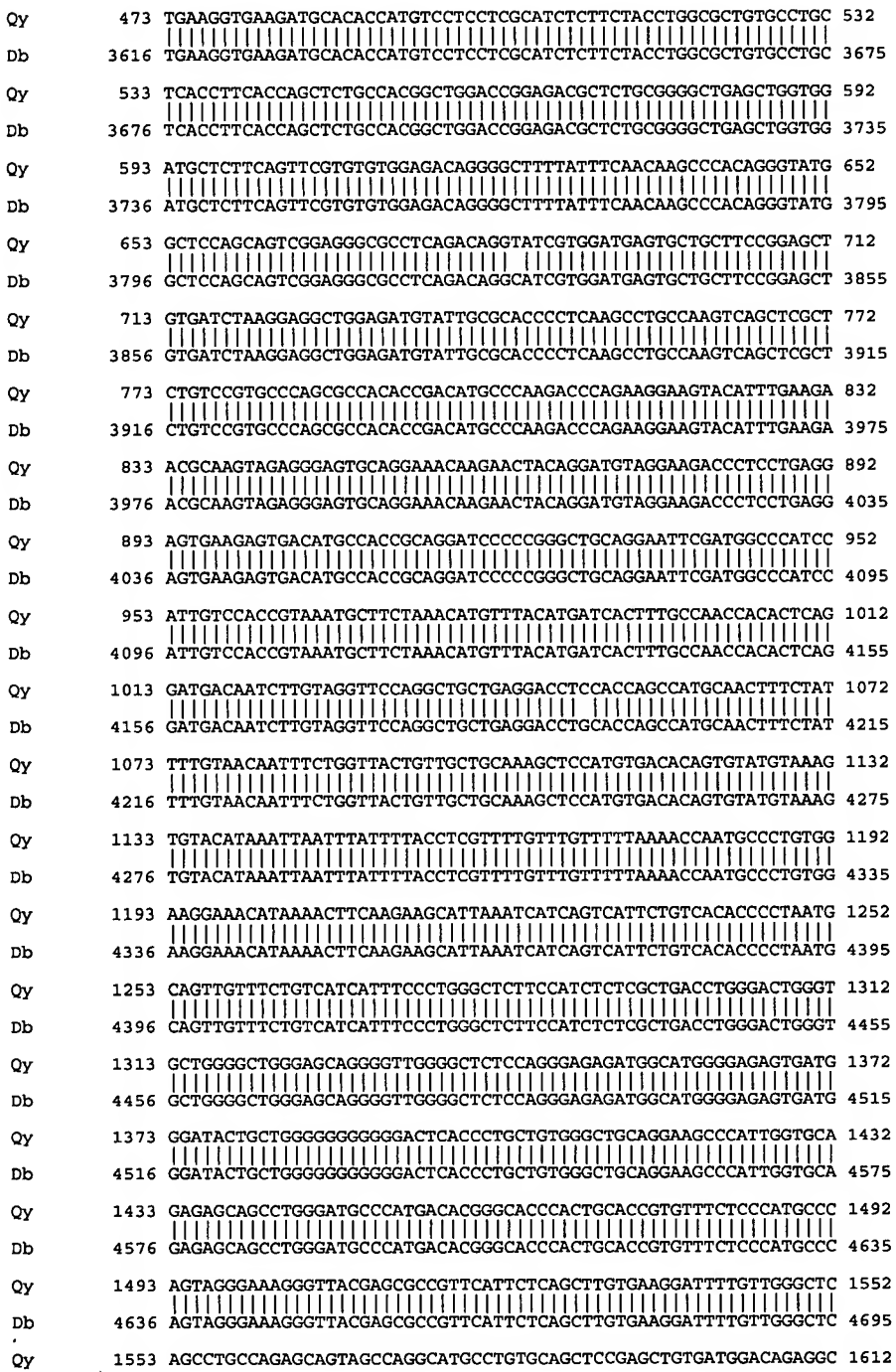
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Db 3616 TGAAGGTGAAGATGCACACCATGTCCTCCTCGCATCTCTTCTACCTGGCGCTGTGCCTGC 3675
Qy 533 TCACCTTCACCAGCTCTGCCACGGCTGGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGG 592
Db 3676 TCACCTTCACCAGCTCTGCCACGGCTGGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGG 3735
Qy 593 ATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTCAACAAGCCCACAGGGTATG 652
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Db 3976 ACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCCTCCTGAGG 4035
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Qy 953 ATTGTCCACCGTAAATGCTTCTAAACATGTTTACATGATCACTTTGCCAACCACACTCAG 1012
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Qy 1253 CAGTTGTTTCTGTCATCATTTCCCTGGGCTCTTCCATCTCTCGCTGACCTGGGACTGGGT 1312
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Qy 1313 GCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGATGGCATGGGGAGAGTGATG 1372
Db 4456 GCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGATGGCATGGGGAGAGTGATG 4515
Qy 1373 GGATACTGCTGGGGGGGGGGGACTCACCCTGCTGTGGGCTGCAGGAAGCCCATTGGTGCA 1432
Db 4516 GGATACTGCTGGGGGGGGGGGACTCACCCTGCTGTGGGCTGCAGGAAGCCCATTGGTGCA 4575
Qy 1433 GAGAGCAGCCTGGGATGCCCATGACACGGGCACCCACTGCACCGTGTTTCTCCCATGCCC 1492
Db 4576 GAGAGCAGCCTGGGATGCCCATGACACGGGCACCCACTGCACCGTGTTTCTCCCATGCCC 4635
Qy 1493 AGTAGGGAAAGGGTTACGAGCGCCGTTCATTCTCAGCTTGTGAAGGATTTTGTTGGGCTC 1552
Db 4636 AGTAGGGAAAGGGTTACGAGCGCCGTTCATTCTCAGCTTGTGAAGGATTTTGTTGGGCTC 4695
Qy 1553 AGCCTGCCAGAGCAGTAGCCAGGCATGCCTGTGCAGCTCCGAGCTGTGATGGACAGAGGC 1612
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Db 4816 TATGGAAAGCCCTCCTGCACTCACCCTGTCCCTGGGGCTGGGGGCAGCCAGGGCCACTTC 4875
Qy 1733 CTCACCCCACCTGACACACAAGGCTTTGCCTGCACAGCCAGGACCTCCTGTGGCCACAGA 1792
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Qy 1793 CTCTTATAGATTCGCTGTGCCCTAGGAGACCAGGGGGCTTTCCCTGCCTGGCCTTCTGGC 1852
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Db 4996 CCCGGCGACACTGCAGGAGCTGCCCTATCTGCCTCCTCTTAGATGGTCCTGGCAGGAAGG 5055
Qy 1913 CTGCACTTGGCTTGGGGCTGATCCATATTACCACTGCAGTAGGGACAGCACTGCTGGAAG 1972
Db 5056 CTGCACTTGGCTTGGGGCTGATCCATATTACCACTGCAGTAGGGACAGCACTGCTGGAAG 5115
Qy 1973 AAAAGATGATTTTCAACTGAACTTACTATCCAGGCAGGTTATTGCTTTATTGTGATGGTG 2032
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Qy 2393 GTGATTGTAGAATCAGTAAGGCTGGAAAAGACCACAGATCATTAAGTCCAACTGTCAGCC 2452
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Qy 2633 GATGTGGTTGCTGAATCAGTACGTTGAGATGTCACTAAACTTTTTGGAGATTAATTTCAG 2692

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Db       5776 GATGTGGTTGCTGAATCAGTACGTTGAGATGTCACTAAACTTTTTGGAGATTAATTTCAG 5835

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Db       5896 TTGCAGGAAAAGATTGTTTGGGAACAGATGAATGGAATTTCCACCAAACAGAAAATTAAC 5955

Qy       2813 ACTTACACCAGTTTGAGTCTGGTCTTCGTTCGATATTTCTTAAGAATCTCATCATCCTCC 2872
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       5956 ACTTACACCAGTTTGAGTCTGGTCTTCGTTGGATATTTCTTAAGAATCTCATCATCCTCC 6015

Qy       2873 CTGCTCTTGGACCAGTGCTGCTGACAGGAGGTGGAGGATCATCAGGGTCAGCATCCTCAG 2932
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2993 GGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA 3052
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3113 GCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGTGGCTGGGAGGCAGCTCTGG 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6256 GCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGTGGCTGGGAGGCAGCTCTGG 6315

Qy       3173 TCCTGGGGTGCTGCAGTGAGCCAGGGAACA 3202
             |||||||||||||||||||||||||||||
Db       6316 TCCTGGGGTGCTGCAGTGAGCCAGGGAACA 6345
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RESULT 4
ADS73977
ID ADS73977 standard; DNA; 2237 BP.
XX
AC ADS73977;
XX
DT 16-DEC-2004 (first entry)
XX
DE Skeletal alpha-actin 3'-end nucleotide fragment.
XX
KW IGF-I; insulin-like growth factor I; myogenic promoter; MEF-1; MEF-2;
KW TEF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis;
KW vascular endothelial growth factor; VEGF; VEGF receptor; antidiabetic;
KW cardiant; vasotropic; ophthalmological; cerebroprotective; ds.
XX
OS Synthetic.
XX
PN WO2004081040-A2.
XX
PD 23-SEP-2004.
XX
PF 11-MAR-2004; 2004WO-US007295.
XX
PR 12-MAR-2003; 2003US-0454079P.
XX
PA (ADVI-) ADVISYS INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Rabinovsky ED, Draghia-Akli R;
XX
DR WPI; 2004-668935/65.
XX
PT New isolated nucleic acid expression construct having a myogenic
PT promoter, a nucleic acid sequence encoding IGF-Ile, and a 3'UTR, useful
PT for treating diabetes, ischemic heart and cerebrovascular disease.
XX
PS Claim 6; SEQ ID NO 5; 104pp; English.
XX
CC The invention relates to an isolated nucleic acid expression construct
CC comprising a myogenic promoter, a nucleic acid sequence encoding an
CC insulin-like growth factor I (IGF-I) or its functional biological
CC equivalent, and a 3' untranslated region (3'UTR), which has in vivo
CC expression activity for the encoded IGF-I in a tissue. The myogenic
CC promoter in the isolated nucleic acid expression construct comprises a
CC transcriptional loci from a family of MEF-1, MEF-2, TEF-1, SRE or SP. The
CC 3'UTR is from a skeletal alpha actin gene or from a human growth hormone.
CC The expression construct further comprises transfection-facilitating
CC vector system that is a plasmid, a viral vector, a liposome, or a
CC cationic lipid. The isolated nucleic acid expression construct also
CC comprises a transfection-facilitating polypeptide having a charged
CC polypeptide and/or poly-L-glutamate. The construct is useful in a method
CC for stimulating angiogenesis, or stimulating myogenesis, or elevating
CC levels of an angiogenic factor, or stimulating endogenous production of
CC an angiopoietin, or treating a muscular or vascular complications of
CC diabetes in a subject. The angiogenic factor comprises a vascular
CC endothelial growth factor (VEGF) or VEGF receptor. The methods and
CC compositions of the present invention are useful for the prevention
CC and/or treatment of diseases or conditions associated with aberrant
CC expression or activity of the IGF-I, such as diabetes mellitus, ischaemic
CC heart disease, diabetic retinopathy and cerebrovascular disease. The
CC present sequence represents the nucleotide sequence of a skeletal alpha-
CC actin 3'-end fragment, a specific example of the 3'- UTR fragment used in
CC the nucleic acid expression construct of the invention.
XX
SQ Sequence 2237 BP; 514 A; 567 C; 569 G; 587 T; 0 U; 0 Other;

Query Match 41.3%; Score 2237; DB 13; Length 2237;
Best Local Similarity 100.0%; Pred. No. 1.5e-278;
Matches 2237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        934 GGAATTCGATGGCCCATCCATTGTCCACCGTAAATGCTTCTAAACATGTTTACATGATCA 993
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Db          1 GGAATTCGATGGCCCATCCATTGTCCACCGTAAATGCTTCTAAACATGTTTACATGATCA 60

Qy        994 CTTTGCCAACCACACTCAGGATGACAATCTTGTAGGTTCCAGGCTGCTGAGGACCTCCAC 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTTTGCCAACCACACTCAGGATGACAATCTTGTAGGTTCCAGGCTGCTGAGGACCTCCAC 120

Qy       1054 CAGCCATGCAACTTTCTATTTTGTAACAATTTCTGGTTACTGTTGCTGCAAAGCTCCATG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGCCATGCAACTTTCTATTTTGTAACAATTTCTGGTTACTGTTGCTGCAAAGCTCCATG 180

Qy       1114 TGACACAGTGTATGTAAAGTGTACATAAATTAATTTATTTACCTCGTTTTGTTTGTTTT 1173
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Db        181 TGACACAGTGTATGTAAAGTGTACATAAATTAATTTATTTACCTCGTTTTGTTTGTTTT 240

Qy       1174 TAAAACCAATGCCCTGTGGAAGGAAACATAAAACTTCAAGAAGCATTAAATCATCAGTCA 1233
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Db        241 TAAAACCAATGCCCTGTGGAAGGAAACATAAAACTTCAAGAAGCATTAAATCATCAGTCA 300

Qy       1234 TTCTGTCACACCCCTAATGCAGTTGTTTCTGTCATCATTTCCCTGGGCTCTTCCATCTCT 1293
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Db        301 TTCTGTCACACCCCTAATGCAGTTGTTTCTGTCATCATTTCCCTGGGCTCTTCCATCTCT 360

Qy       1294 CGCTGACCTGGGACTGGGTGCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGA 1353
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Db        361 CGCTGACCTGGGACTGGGTGCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGA 420

Qy       1354 TGGCATGGGGAGAGTGATGGGATACTGCTGGGGGGGGGGGGACTCACCCTGCTGTGGGCTG 1413
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Db        421 TGGCATGGGGAGAGTGATGGGATACTGCTGGGGGGGGGGGGACTCACCCTGCTGTGGGCTG 480

Qy       1414 CAGGAAGCCCATTGGTGCAGAGAGCAGCCTGGGATGCCCATGACACGGGCACCCACTGCA 1473
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Qy       1474 CCGTGTTTCTCCCATGCCCAGTAGGGAAAGGGTTACGAGCGCCGTTCATTCTCAGCTTGT 1533
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Qy       1654 AAGAGCTTTCCACTCCACTTATGGAAAGCCCTCCTGCACTCACCCTGTCCCTGGGGCTGG 1713
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Db        721 AAGAGCTTTCCACTCCACTTATGGAAAGCCCTCCTGCACTCACCCTGTCCCTGGGGCTGG 780

Qy       1714 GGGCAGCCAGGGCCACTTCCTCACCCCACCTGACACACAAGGCTTTGCCTGCACAGCCAG 1773
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Qy       1774 GACCTCCTGTGGCCACAGACTCTTATAGATTCGCTGTGCCCTAGGAGACCAGGGGGCTTT 1833
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Db        841 GACCTCCTGTGGCCACAGACTCTTATAGATTCGCTGTGCCCTAGGAGACCAGGGGGCTTT 900

Qy       1834 CCCTGCCTGGCCTTCTGGCCCCGGCGACACTGCAGGAGCTGCCCTATCTGCCTCCTCTTA 1893
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Qy       1894 GATGGTCCTGGCAGGAAGGCTGCACTTGGCTTGGGGCTGATCCATATTACCACTGCAGTA 1953
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Db        961 GATGGTCCTGGCAGGAAGGCTGCACTTGGCTTGGGGCTGATCCATATTACCACTGCAGTA 1020

Qy       1954 GGGACAGCACTGCTGGAAGAAAAGATGATTTTCAACTGAACTTACTATCCAGGCAGGTTA 2013
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Db       1021 GGGACAGCACTGCTGGAAGAAAAGATGATTTTCAACTGAACTTACTATCCAGGCAGGTTA 1080

Qy       2014 TTGCTTTATTGTGATGGTGCTAAGAGTGCGTTCTTTCTCACTGTAATGATTTTGCCCTCA 2073
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Db       1081 TTGCTTTATTGTGATGGTGCTAAGAGTGCGTTCTTTCTCACTGTAATGATTTTGCCCTCA 1140

Qy       2074 TGTGTGAATACACTTTCCAATAACAGCACAGCCTCCAAAGGGAATTTCTGCAGGAAGAGA 2133
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Db       1141 TGTGTGAATACACTTTCCAATAACAGCACAGCCTCCAAAGGGAATTTCTGCAGGAAGAGA 1200

Qy       2134 CAGTACCTGGTGTGGGAAGTCCCTGTGCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGA 2193
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Db       1201 CAGTACCTGGTGTGGGAAGTCCCTGTGCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGA 1260

Qy       2194 CTGGCTGGGAGAGCAGGATCACATCCTTTCTTAAAAAGACAAACAGAAGGTAGTGTGTGA 2253
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Db       1261 CTGGCTGGGAGAGCAGGATCACATCCTTTCTTAAAAAGACAAACAGAAGGTAGTGTGTGA 1320

Qy       2254 CCTTGCTGTATTTACTATTTACGCGTTGTTGTTCAGTGGCACATACCTCAACGGGGATAT 2313
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Qy       2314 GGAGAGCTATTTCCCCAACCCTCGCTGCTGGACCCTGATCTGGGGTTTTCCTGTAGCTTA 2373
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Qy       2374 AGCGGTGCCAACTGCTTAAGTGATTGTAGAATCAGTAAGGCTGGAAAAGACCACAGATCA 2433
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Qy       2434 TTAAGTCCAACTGTCAGCCCCATCCCCACCGCGCCCACTGTCACTCAGTGCCACATCCAC 2493
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Qy       2554 AGGCAGGGTGACAGTCTCAGTGCCAGTTGCATCCTGCTGAAGAGCTTAACAGTGCAGTTT 2613
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Db       1621 AGGCAGGGTGACAGTCTCAGTGCCAGTTGCATCCTGCTGAAGAGCTTAACAGTGCAGTTT 1680

Qy       2614 AACAACGGACTGATTTGTTGATGTGGTTGCTGAATCAGTACGTTGAGATGTCACTAAACT 2673
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Qy       2674 TTTTGGAGATTAATTTCAGGATGGAACACATTCTTAACCCTGAAACCAGCCTTTGATTTG 2733
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Qy       2734 GGCTTGGCATTTGCAGAATTTGCAGGAAAAGATTGTTTGGGAACAGATGAATGGAATTTC 2793
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Db       1801 GGCTTGGCATTTGCAGAATTTGCAGGAAAAGATTGTTTGGGAACAGATGAATGGAATTTC 1860

Qy       2794 CACCAAACAGAAAATTAACACTTACACCAGTTTGAGTCTGGTCTTCGTTCGATATTTCTT 2853
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Db       1861 CACCAAACAGAAAATTAACACTTACACCAGTTTGAGTCTGGTCTTCGTTCGATATTTCTT 1920

Qy       2854 AAGAATCTCATCATCCTCCCTGCTCTTGGACCAGTGCTGCTGACAGGAGGTGGAGGATCA 2913
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Db       1921 AAGAATCTCATCATCCTCCCTGCTCTTGGACCAGTGCTGCTGACAGGAGGTGGAGGATCA 1980

Qy       2914 TCAGGGTCAGCATCCTCAGCATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGA 2973
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Db       1981 TCAGGGTCAGCATCCTCAGCATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGA 2040

Qy       2974 GAACTGCTTTGATTCCCCAGGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCT 3033
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Db       2041 GAACTGCTTTGATTCCCCAGGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCT 2100

Qy       3034 GAAAGTCCAACTTTCTGAACTTCCAGCACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGG 3093
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Db       2101 GAAAGTCCAACTTTCTGAACTTCCAGCACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGG 2160

Qy       3094 CCACAGGGACTGTAGCCAGGCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGT 3153
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Db       2161 CCACAGGGACTGTAGCCAGGCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGT 2220

Qy       3154 GGCTGGGAGGCAGCTCT 3170
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Db       2221 GGCTGGGAGGCAGCTCT 2237
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RESULT 5
AAV50428
ID   AAV50428 standard; DNA; 3599 BP.
XX
AC   AAV50428;
XX
DT   26-OCT-1998  (first entry)
XX
DE   Plasmid pIG0552 lower sequence nucleotides 1-3599.
XX
KW   Human; IGF-1; insulin-like growth factor 1; urinary incontinence;
KW   gene therapy; neurotrophic factor; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9833529-A1.
XX
PD   06-AUG-1998.
XX
PF   04-FEB-1998;   98WO-US002051.
XX
PR   04-FEB-1997;   97US-0036862P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Coleman M;
XX
DR   WPI; 1998-437184/37.
XX
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PT Treatment of urinary incontinence - by delivering nucleic acid vector for
PT expression of growth factor or neurotrophic factor in tissue(s).
XX
PS Disclosure; Page 105-107; 117pp; English.
XX
CC A method has been developed of treating urinary incontinence (UI) in
CC mammals. The method comprises delivering a nucleic acid vector for the
CC expression of a growth factor or neurotrophic factor in a tissue or
CC tissues. The present sequence represents the actual lower sequence of
CC plasmid pIG0552 nucleotides 1-3599 from the present invention. Due to the
CC growth and stimulatory effects of growth factors and neurotrophic
CC factors, introducing these factors to degenerated muscles in the urinary
CC system can improve UI by enhancing both their integrity and neural
CC innervation
XX
SQ Sequence 3599 BP; 733 A; 1098 C; 1042 G; 726 T; 0 U; 0 Other;

Query Match 40.9%; Score 2218; DB 2; Length 3599;
Best Local Similarity 99.6%; Pred. No. 3.7e-276;
Matches 2224; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy    3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
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Db       3 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 62

Qy    3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
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Db      63 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 122

Qy    3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
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Db     123 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 182

Qy    3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
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Db     183 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 242

Qy    3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
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Db     243 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 302

Qy    3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
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Db     303 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 362

Qy    3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
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Db     363 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 422

Qy    3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
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Db     423 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 482

Qy    3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
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Db     483 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 542

Qy    3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
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Db     543 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 602

Qy    3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
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Db     603 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 662

Qy    3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
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Db     663 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 722

Qy    3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
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Db     723 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 782

Qy    3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
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Db     783 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 842

Qy    4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
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Db     843 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 902

Qy    4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
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Qy    4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
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Db     963 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 1022

Qy    4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
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Db    1023 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 1082

Qy    4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
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Db    1083 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 1142

Qy    4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
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Db    1143 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 1202

Qy    4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
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Qy    4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
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Db    1263 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 1322

Qy    4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
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Db    1323 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 1382

Qy    4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
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Db    1383 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 1442

Qy    4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
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Db    1443 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 1502

Qy    4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
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Db    1503 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 1562

Qy    4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
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Qy    4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
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Qy    4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
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Db    1683 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 1742

Qy    4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1743 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 1802

Qy    4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1803 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 1862

Qy    5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1863 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 1922

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1923 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 1982

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1983 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 2042

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2043 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 2102

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2103 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 2162

Qy       5350 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 5409
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2163 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 2222

Qy       5410 GGCGAATTGGAGCT 5423
                ||||||||||||||
Db       2223 GGCGAATTGGAGCT 2236


RESULT 6
AAV40796
ID   AAV40796 standard; DNA; 3599 BP.
XX
AC   AAV40796;
XX
DT   23-SEP-1998  (first entry)
XX
DE   Actual sequence of IGF-I containing plasmid pIG0552.
XX
KW   IGF-I; insulin-like growth factor I; skeletal alpha-actin gene promoter;
KW   muscle atrophy; diabetes; osteoporosis; growth disorder; therapy; AIDS;
KW   Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss.
XX
OS   Synthetic.
XX
PN   WO9824922-A1.
XX
PD   11-JUN-1998.
XX
PF   01-DEC-1997;   97WO-US021852.
XX
PR   02-DEC-1996;   96US-0031539P.
PR   19-NOV-1997;   97US-00974572.
XX
PA   (GENE-) GENEMEDICINE INC.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Coleman M,  Schwartz R,  Demayo FJ;
XX
DR   WPI; 1998-333339/29.
XX
PT   New vector for expression of insulin-like growth factor-I - containing a
PT   skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3'
PT   region from growth hormone 3'-UTR.
XX
PS   Claim 16; Page 37-41; 115pp; English.
XX
CC   This sequence is the actual sequence for pIG0552 which is an example of a
CC   vector of the invention. The vector is for expression of a nucleic acid
CC   sequence in a cell, and comprises: (a) a nucleic acid cassette containing
CC   a sequence encoding insulin-like growth factor-I (IGF-I); (b) a 5'
CC   flanking region including one or more sequences necessary for expression
CC   of the nucleic acid cassette, including a promoter from a skeletal alpha-
CC   actin gene; (c) a linker connecting the 5' flanking region to a nucleic
CC   acid, the linker having a position for inserting the nucleic acid
CC   cassette, and lacking the coding sequence of a gene with which it is
CC   naturally associated; and (d) a 3' flanking region, including a 3'
CC   untranslated region or a 3' non coding region or both, where the 3'
CC   flanking region is 3' to the position for inserting the nucleic acid
CC   cassette and comprises a sequence from a growth hormone 3'-UTR. The
CC   vector can provide for efficient IGF-I expression, particularly in gene
CC   therapy. It can be used for the delivery of IGF-I for treating diseases
CC   such as muscle atrophy, diabetes, neuropathy, osteoporosis, and growth
CC   disorders. They can be used for treating peripheral neuropathies
CC   resulting from diabetes, genetic disease such as Type I or Type II
CC   diabetes, genetic disease such as Chacot-marie-tooth disease, AIDS,
CC   atherogenesis, atherosclerotic, cardiovascular, cerebrovascular, or
CC   peripheral vascular disease, haemophilia, inflammation and side-effects
CC   from anti-cancer and anti-viral drugs. The vectors can also be used to
CC   create transgenic animals for research or livestock improvement
XX
SQ   Sequence 3599 BP; 733 A; 1098 C; 1042 G; 726 T; 0 U; 0 Other;

  Query Match             40.9%;  Score 2218;  DB 2;  Length 3599;
  Best Local Similarity   99.6%;  Pred. No. 3.7e-276;
  Matches 2224;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
                |||   |||  |     ||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 62

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          63 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 122

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         123 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 182

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         183 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 242

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         243 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 302

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         303 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 362

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         363 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 422

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         423 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 482

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         483 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 542

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         543 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 602

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         603 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 662

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         663 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 722

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        723 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 782

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 842

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 902

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 962

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 1022

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 1082

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 1142

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 1202

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1203 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 1262

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1263 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 1322

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1323 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 1382

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1383 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 1442

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1443 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 1502

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1503 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 1562

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1563 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 1622

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1623 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 1682

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1683 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 1742

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1743 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 1802

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1803 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 1862

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1863 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 1922

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1923 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 1982

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1983 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 2042

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2043 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 2102

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2103 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 2162

Qy       5350 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 5409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2163 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 2222

Qy       5410 GGCGAATTGGAGCT 5423
              ||||||||||||||
Db       2223 GGCGAATTGGAGCT 2236
```

RESULT 7
ADS73974
ID ADS73974 standard; DNA; 3803 BP.
XX
AC ADS73974;
XX
DT 16-DEC-2004 (first entry)
XX
DE Plasmid pAV2002 nucleotide sequence.
XX
KW IGF-I; insulin-like growth factor I; myogenic promoter; MEF-1; MEF-2;
KW TEF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis;
KW vascular endothelial growth factor; VEGF; VEGF receptor; antidiabetic;
KW cardiant; vasotropic; ophthalmological; cerebroprotective; ds.
XX
OS Synthetic.
XX
PN WO2004081040-A2.
XX
PD 23-SEP-2004.
XX
PF 11-MAR-2004; 2004WO-US007295.
XX
PR 12-MAR-2003; 2003US-0454079P.
XX
PA (ADVI-) ADVISYS INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Rabinovsky ED, Draghia-Akli R;
XX
DR WPI; 2004-668935/65.
XX
PT New isolated nucleic acid expression construct having a myogenic
PT promoter, a nucleic acid sequence encoding IGF-Ile, and a 3'UTR, useful
PT for treating diabetes, ischemic heart and cerebrovascular disease.
XX
PS Claim 11; SEQ ID NO 2; 104pp; English.
XX
CC The invention relates to an isolated nucleic acid expression construct
CC comprising a myogenic promoter, a nucleic acid sequence encoding an
CC insulin-like growth factor I (IGF-I) or its functional biological
CC equivalent, and a 3' untranslated region (3'UTR), which has in vivo
CC expression activity for the encoded IGF-I in a tissue. The myogenic

CC promoter in the isolated nucleic acid expression construct comprises a
CC transcriptional loci from a family of MEF-1, MEF-2, TEF-1, SRE or SP. The
CC 3'UTR is from a skeletal alpha actin gene or from a human growth hormone.
CC The expression construct further comprises transfection-facilitating
CC vector system that is a plasmid, a viral vector, a liposome, or a
CC cationic lipid. The isolated nucleic acid expression construct also
CC comprises a transfection-facilitating polypeptide having a charged
CC polypeptide and/or poly-L-glutamate. The construct is useful in a method
CC for stimulating angiogenesis, or stimulating myogenesis, or elevating
CC levels of an angiogenic factor, or stimulating endogenous production of
CC an angiopoietin, or treating a muscular or vascular complications of
CC diabetes in a subject. The angiogenic factor comprises a vascular
CC endothelial growth factor (VEGF) or VEGF receptor. The methods and
CC compositions of the present invention are useful for the prevention
CC and/or treatment of diseases or conditions associated with aberrant
CC expression or activity of the IGF-I, such as diabetes mellitus, ischaemic
CC heart disease, diabetic retinopathy and cerebrovascular disease. The
CC present sequence represents the nucleotide sequence of a plasmid pAV2002,
CC a specific example of the isolated nucleic acid expression construct of
CC the invention.
XX
SQ Sequence 3803 BP; 828 A; 1075 C; 1063 G; 837 T; 0 U; 0 Other;

Query Match 40.9%; Score 2218; DB 13; Length 3803;
Best Local Similarity 99.6%; Pred. No. 3.6e-276;
Matches 2224; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             ||| ||| |     ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1629

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1689

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1749

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1750 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1809

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1810 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1869

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1870 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1929

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1930 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1989

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1990 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 2049

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2050 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 2109

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2110 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 2169

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2170 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2229

.Qy      3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       2230 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 2289

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2290 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 2349

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2409

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2469

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2529

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2589

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2590 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2649

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2709

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2769

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2770 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2829

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2830 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2889

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2890 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2949

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2950 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 3009

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3010 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 3069

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 3129

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 3189

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3190 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 3249

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3309

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3310 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 3369
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Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3370 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3429

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3430 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3489

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3490 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3549

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3550 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3609

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3610 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3669

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3670 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3729

Qy       5350 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 5409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3730 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 3789

Qy       5410 GGCGAATTGGAGCT 5423
             ||||||||||||||
Db       3790 GGCGAATTGGAGCT 3803
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RESULT 8
AAV50427
ID AAV50427 standard; DNA; 3600 BP.
XX
AC AAV50427;
XX
DT 26-OCT-1998 (first entry)
XX
DE Plasmid pIG0552 upper expected sequence nucleotides 1-3600.
XX
KW Human; IGF-1; insulin-like growth factor 1; urinary incontinence;
KW gene therapy; neurotrophic factor; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9833529-A1.
XX
PD 06-AUG-1998.
XX
PF 04-FEB-1998; 98WO-US002051.
XX
PR 04-FEB-1997; 97US-0036862P.
XX
PA (GENE-) GENEMEDICINE INC.
XX
PI Coleman M;
XX
DR WPI; 1998-437184/37.
XX
PT Treatment of urinary incontinence - by delivering nucleic acid vector for
PT expression of growth factor or neurotrophic factor in tissue(s).
XX
PS Disclosure; Page 103-105; 117pp; English.
XX
CC A method has been developed of treating urinary incontinence (UI) in
CC mammals. The method comprises delivering a nucleic acid vector for the
CC expression of a growth factor or neurotrophic factor in a tissue or
CC tissues. The present sequence represents the expected upper sequence of
CC plasmid pIG0552 nucleotides 1-3600 from the present invention. Due to the
CC growth and stimulatory effects of growth factors and neurotrophic
CC factors, introducing these factors to degenerated muscles in the urinary
CC system can improve UI by enhancing both their integrity and neural
CC innervation
XX
SQ Sequence 3600 BP; 733 A; 1099 C; 1042 G; 726 T; 0 U; 0 Other;

```
  Query Match             40.9%;  Score 2215.8;  DB 2;  Length 3600;
  Best Local Similarity   99.9%;  Pred. No. 7e-276;
  Matches 2217;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3205 CTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAG 3264
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 CCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAG 78

Qy       3265 CTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGC 3324
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 CTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGC 138

Qy       3325 ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGC 3384
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGC 198

Qy       3385 TCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA 3444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA 258

Qy       3445 CGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG 3504
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG 318

Qy       3505 CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG 3564
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG 378

Qy       3565 TTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG 3624
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 TTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG 438

Qy       3625 GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC 3684
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC 498

Qy       3685 GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA 3744
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA 558

Qy       3745 TACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTT 3804
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTT 618

Qy       3805 ACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC 3864
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC 678

Qy       3865 TGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC 3924
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 TGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC 738

Qy       3925 CCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA 3984
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 CCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA 798

Qy       3985 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT 4044
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT 858

Qy       4045 GTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA 4104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        859 GTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACA 918

Qy       4105 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT 4164
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Db        919 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT 978

Qy       4165 TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATT 4224

Db        979 TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATT 1038

Qy       4225 ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCT 4284

Db       1039 ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCT 1098

Qy       4285 CAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATA 4344

Db       1099 CAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATA 1158

Qy       4345 CCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGG 4404

Db       1159 CCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGG 1218

Qy       4405 GTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAAT 4464

Db       1219 GTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAAT 1278

Qy       4465 CCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACG 4524

Db       1279 CCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACG 1338

Qy       4525 ACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCG 4584

Db       1339 ACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCG 1398

Qy       4585 AGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTA 4644

Db       1399 AGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTA 1458

Qy       4645 CGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGC 4704

Db       1459 CGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGC 1518

Qy       4705 GTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGA 4764

Db       1519 GTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGA 1578

Qy       4765 GATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCA 4824

Db       1579 GATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCA 1638

Qy       4825 GTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGC 4884

Db       1639 GTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGC 1698

Qy       4885 GCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACC 4944

Db       1699 GCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACC 1758

Qy       4945 GGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGT 5004

Db       1759 GGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGT 1818

Qy       5005 GCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCA 5064

Db       1819 GCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCA 1878

Qy       5065 TCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTG 5124

Db       1879 TCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTG 1938

Qy       5125 CGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACC 5184

Db       1939 CGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACC 1998

Qy       5185 TTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAG 5244

Db       1999 TTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAG 2058

Qy       5245 TCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCG 5304

Db       2059 TCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCG 2118

Qy       5305 AAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGA 5364

Db       2119 AAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGA 2178

Qy       5365 CGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGAGCT 5423

Db       2179 CGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGAGCT 2237
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RESULT 9
AAV40795
ID AAV40795 standard; DNA; 3600 BP.
XX
AC AAV40795;
XX
DT 23-SEP-1998 (first entry)
XX
DE Expected sequence of IGF-I containing plasmid pIG0552.
XX
KW IGF-I; insulin-like growth factor I; skeletal alpha-actin gene promoter;
KW muscle atrophy; diabetes; osteoporosis; growth disorder; therapy; AIDS;
KW Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss.
XX
OS Synthetic.
XX
PN WO9824922-A1.
XX
PD 11-JUN-1998.
XX
PF 01-DEC-1997; 97WO-US021852.
XX
PR 02-DEC-1996; 96US-0031539P.
PR 19-NOV-1997; 97US-00974572.
XX
PA (GENE-) GENEMEDICINE INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Coleman M, Schwartz R, Demayo FJ;
XX
DR WPI; 1998-333339/29.
XX
PT New vector for expression of insulin-like growth factor-I - containing a
PT skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3'
PT region from growth hormone 3'-UTR.
XX
PS Claim 16; Page 37-41; 115pp; English.
XX
CC This sequence is the expected sequence for pIG0552 which is an example of
CC a vector of the invention. The vector is for expression of a nucleic acid
CC sequence in a cell, and comprises: (a) a nucleic acid cassette containing
CC a sequence encoding insulin-like growth factor-I (IGF-I); (b) a 5'
CC flanking region including one or more sequences necessary for expression
CC of the nucleic acid cassette, including a promoter from a skeletal alpha-
CC actin gene; (c) a linker connecting the 5' flanking region to a nucleic
CC acid, the linker having a position for inserting the nucleic acid
CC cassette, and lacking the coding sequence of a gene with which it is
CC naturally associated; and (d) a 3' flanking region, including a 3'
CC untranslated region or a 3' non coding region or both, where the 3'
CC flanking region is 3' to the position for inserting the nucleic acid
CC cassette and comprises a sequence from a growth hormone 3'-UTR. The
CC vector can provide for efficient IGF-I expression, particularly in gene
CC therapy. It can be used for the delivery of IGF-I for treating diseases
CC such as muscle atrophy, diabetes, neuropathy, osteoporosis, and growth
CC disorders. They can be used for treating peripheral neuropathies
CC resulting from diabetes, genetic disease such as Type I or Type II
CC diabetes, genetic disease such as Chacot-marie-tooth disease, AIDS,
CC atherogenesis, atherosclerotic, cardiovascular, cerebrovascular, or

CC peripheral vascular disease, haemophilia, inflammation and side-effects
CC from anti-cancer and anti-viral drugs. The vectors can also be used to
CC create transgenic animals for research or livestock improvement
XX
SQ Sequence 3600 BP; 733 A; 1099 C; 1042 G; 726 T; 0 U; 0 Other;

Query Match 40.9%; Score 2215.8; DB 2; Length 3600;
Best Local Similarity 99.9%; Pred. No. 7e-276;
Matches 2217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    3205 CTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAG 3264
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19 CCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAG 78

Qy    3265 CTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGC 3324
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79 CTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGC 138

Qy    3325 ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGC 3384
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     139 ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGC 198

Qy    3385 TCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA 3444
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     199 TCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA 258

Qy    3445 CGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG 3504
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     259 CGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG 318

Qy    3505 CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG 3564
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     319 CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG 378

Qy    3565 TTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG 3624
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     379 TTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG 438

Qy    3625 GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC 3684
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     439 GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC 498

Qy    3685 GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA 3744
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     499 GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA 558

Qy    3745 TACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTT 3804
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     559 TACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTT 618

Qy    3805 ACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC 3864
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     619 ACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC 678

Qy    3865 TGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC 3924
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     679 TGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC 738

Qy    3925 CCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA 3984
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     739 CCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA 798

Qy    3985 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT 4044
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     799 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT 858

Qy    4045 GTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA 4104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     859 GTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACA 918

Qy    4105 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT 4164
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     919 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT 978

Qy    4165 TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATT 4224
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     979 TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATT 1038

Qy    4225 ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCT 4284
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1039 ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCT 1098

Qy    4285 CAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATA 4344
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1099 CAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATA 1158

Qy    4345 CCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGG 4404
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1159 CCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGG 1218

Qy    4405 GTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAAT 4464
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1219 GTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAAT 1278

Qy    4465 CCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACG 4524
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1279 CCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACG 1338

Qy    4525 ACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCG 4584
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1339 ACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCG 1398

Qy    4585 AGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTA 4644
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1399 AGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTA 1458

Qy    4645 CGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGC 4704
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1459 CGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGC 1518

Qy    4705 GTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGA 4764
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1519 GTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGA 1578

Qy    4765 GATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCA 4824
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1579 GATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCA 1638

Qy    4825 GTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGC 4884
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1639 GTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGC 1698

Qy    4885 GCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACC 4944
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1699 GCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACC 1758

Qy    4945 GGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGT 5004
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1759 GGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGT 1818

Qy    5005 GCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCA 5064
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1819 GCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCA 1878

Qy    5065 TCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTG 5124
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1879 TCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTG 1938

Qy    5125 CGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACC 5184
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1939 CGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACC 1998

Qy    5185 TTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAG 5244
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1999 TTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAG 2058
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Qy       5245 TCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCG 5304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2059 TCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCG 2118

Qy       5305 AAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGA 5364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2119 AAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGA 2178

Qy       5365 CGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGAGCT 5423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2179 CGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGAGCT 2237


RESULT 10
AAL60457
ID   AAL60457 standard; DNA; 3558 BP.
XX
AC   AAL60457;
XX
DT   27-AUG-2003  (first entry)
XX
DE   pGR1774 plasmid comprising human (1-40) GHRH DNA.
XX
KW   Growth hormone releasing hormone; GHRH; lean body mass; bone density;
KW   bone healing; gene therapy; anorectic; osteopathic; circular; cyclic;
KW   human; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003038112-A2.
XX
PD   08-MAY-2003.
XX
PF   25-OCT-2002; 2002WO-US034275.
XX
PR   26-OCT-2001; 2001US-0357808P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Draghia-Akli R,  Schwartz RJ;
XX
DR   WPI; 2003-493212/46.
XX
PT   Decreasing body fat proportion, increasing lean body mass, bone density
PT   or bone healing rate by delivering into cells of the subject a nucleic
PT   acid expression construct that encodes a growth-hormone-releasing-hormone
PT   (GHRH).
XX
PS   Claim 30; Page 160-162; 165pp; English.
XX
CC   The invention relates to a method for decreasing body fat proportion,
CC   increasing lean body mass, bone density or bone healing rate in a subject
CC   which involves delivering a nucleic acid expression construct that
CC   encodes a growth hormone releasing hormone (GHRH) or its functional
CC   biological equivalent into cells of the subject. The method is useful for
CC   decreasing body fat proportion, for increasing lean body mass, bone
CC   density or bone healing rate, or for altering lean body mass in a
CC   subject. It is used in gene therapy. The present sequence is a pGR1774
CC   plasmid comprising human (1-40) GHRH DNA. This sequence is used to
CC   illustrate the method of the invention
XX
SQ   Sequence 3558 BP; 774 A; 1018 C; 949 G; 816 T; 0 U; 1 Other;

  Query Match           40.8%;  Score 2211.6;  DB 9;  Length 3558;
  Best Local Similarity  99.5%;  Pred. No. 2.4e-275;
  Matches 2217;  Conservative    1;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             |||   |||  |     ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1259

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1260 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1319

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1379

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1380 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1439

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1440 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1499

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1500 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1559

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1560 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1619

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1620 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1679

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1680 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1739

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1740 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1799

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1800 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 1859

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1860 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 1919

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1920 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 1979

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1980 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2039

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2040 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2099

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2100 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2159

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2160 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2219

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2220 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2279

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2280 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2339

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2340 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2399
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Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2400 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2459

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2460 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2519

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2520 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2579

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2580 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2639

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
             ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2640 GCTTCCATYCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2699

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2700 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2759

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2760 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2819

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2820 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 2879

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2880 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 2939

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2940 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 2999

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3000 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3059

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3060 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3119

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3120 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3179

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3180 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3239

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3240 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3299

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3300 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3359

Qy       5350 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 5409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3360 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 3419

Qy       5410 GGCGAATT 5417
             ||||||||
Db       3420 GGCGAATT 3427
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RESULT 11
ADR23406
ID   ADR23406 standard; DNA; 3558 BP.
XX
AC   ADR23406;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Inducible pGR1774 encoding human growth hormone releasing hormone.
XX
KW   Growth hormone releasing hormone; GHRH; human; pGR1774; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004067719-A2.
XX
PD   12-AUG-2004.
XX
PF   26-JAN-2004; 2004WO-US002134.
XX
PR   28-JAN-2003; 2003US-0443104P.
XX
PA   (ADVI-) ADVISYS INC.
XX
PI   Brown PA,  Draghia-Akli R,  Carpenter RH;
XX
DR   WPI; 2004-594202/57.
XX
PT   Decreasing an involuntary cull in farm animals comprises delivering into
PT   a tissue of the farm animals an isolated nucleic acid expression
PT   construct encoding a growth-hormone-releasing-hormone (GHRH) or its
PT   functional equivalent.
XX
PS   Disclosure; SEQ ID NO 26; 135pp; English.
XX
CC   The present sequence is that of inducible plasmid pGR1774 encoding human
CC   growth hormone releasing hormone (GHRH). The invention relates to methods
CC   of decreasing voluntary cull rates in farm animals resulting from
CC   infection, disease, morbidity or mortality, of increasing milk production
CC   in dairy cows, and of increasing body condition scores in farm animals by
CC   delivering a nucleic acid expression construct that encodes a GHRH or its
CC   functional biological equivalent. The expression construct is delivered
CC   by electroporation, via a viral vector, in conjunction with a carrier, by
CC   a parenteral route, or a combination of these. Electroporation may be
CC   used to deliver the nucleic acid construct in a single dose, into diploid
CC   (e.g. muscle) cells, with demonstrated long-term effects. The farm animal
CC   may be a ruminant, food or work animal, e.g. a pig, dairy cow, sheep,
CC   goat or chicken. The involuntary cull comprises mortality at birth or of
CC   newborns. Delivery of the nucleic acid expression construct decreases
CC   involuntary cull in farm animals from about 20% to less than 15%.
XX
SQ   Sequence 3558 BP; 774 A; 1018 C; 949 G; 816 T; 0 U; 1 Other;

  Query Match             40.8%;  Score 2211.6;  DB 13;  Length 3558;
  Best Local Similarity   99.5%;  Pred. No. 2.4e-275;
  Matches 2217;  Conservative    1;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             |||   |||  |     ||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1259

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1260 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1319

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1379

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1380 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1439
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Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1440 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1499

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1500 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1559

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1560 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1619

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1620 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1679

Qy       3670 CTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1680 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1739

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1740 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1799

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1800 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 1859

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1860 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 1919

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1920 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 1979

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1980 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2039

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2040 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2099

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2100 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2159

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2160 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2219

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2220 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2279

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2280 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2339

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2340 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2399

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2400 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2459

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2460 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2519

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2520 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2579

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2580 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2639

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
             ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2640 GCTTCCATYCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2699

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2700 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2759

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2760 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2819

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2820 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 2879

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2880 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 2939

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2940 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 2999

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3000 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3059

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3060 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3119

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3120 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3179

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3180 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3239

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3240 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3299

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3300 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3359

Qy       5350 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 5409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3360 TTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG 3419

Qy       5410 GGCGAATT 5417
             ||||||||
Db       3420 GGCGAATT 3427
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RESULT 12
ABQ78294
ID   ABQ78294 standard; DNA; 2192 BP.
XX
AC   ABQ78294;
XX
DT   05-NOV-2002  (first entry)
XX
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DE Nucleotide sequence of plasmid pVC0289.
XX
KW Pig; growth hormone releasing hormone; GHRH; growth rate; lean body mass;
KW Insulin-like Growth Factor-I; IGF-I; milk production; feed efficiency;
KW somatotroph; growth-related disorder; hypopituitary dwarfism;
KW meat production; egg production; ss.
XX
OS Synthetic.
XX
PN WO200261037-A2.
XX
PD 08-AUG-2002.
XX
PF 12-DEC-2001; 2001WO-US048726.
XX
PR 12-DEC-2000; 2000US-0255021P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (ADVI-) ADVISYS.
XX
PI Schwartz RJ, Carpenter RH, Draghia-Akli R, Kern DR, Smith RG;
XX
DR WPI; 2002-619237/66.
XX
PT Improving or enhancing growth, lean body mass, milk production, feed
PT efficiency or Insulin-like Growth Factor-I levels, comprises introducing
PT a vector encoding a growth hormone releasing hormone into an animal
PT before or during gestation.
XX
PS Example 2; Page 111-112; 113pp; English.
XX
CC The present sequence represents plasmid pVC0289, which was used to create
CC a vector carrying cDNA encoding pig growth hormone releasing hormone
CC (GHRH) cDNA. Nucleic acids encoding GHRH are used in the method of the
CC invention. The specification describes a method for improving or
CC enhancing characteristics e.g. growth, lean body mass, Insulin-like
CC Growth Factor (IGF)-I levels, growth rate and milk production in an
CC offspring, and for delaying birth of an offspring. The method comprises
CC introducing a vector, encoding GHRH, into cells of the female animal
CC prior to or during gestation of the offspring under conditions where the
CC nucleotide sequence is expressed. The method is useful of improving or
CC enhancing animal growth, for increasing growth hormone, lean body mass,
CC IGF-I levels, feed efficiency, growth rate, ratio of somatotrophs to
CC other hormone-producing cells in a pituitary gland, and milk production
CC in an offspring, and for delaying birth of an offspring. GHRH nucleic
CC acids and vectors are used for diagnostic purposes in clinical medicine,
CC both human and veterinary, e.g. in treating growth-related disorders such
CC as hypopituitary dwarfism resulting from abnormalities in growth hormone
CC production, and in stimulating the growth and enhancing feed conversion
CC efficiency of animals raised for meat, milk and egg production
XX
SQ Sequence 2192 BP; 486 A; 634 C; 601 G; 471 T; 0 U; 0 Other;

Query Match 39.8%; Score 2160; DB 6; Length 2192;
Best Local Similarity 99.5%; Pred. No. 1.1e-268;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             ||| ||| |     ||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 76

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 136

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 196

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 256

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 316

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 376

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 436

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 496

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 556

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 616

Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 676

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 736

Qy       3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 796

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 856

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 916

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 976

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 1036

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 1096

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 1156

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1157 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 1216

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1217 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 1276

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1277 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 1336

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
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Db       1337 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 1396

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1397 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 1456

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1457 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 1516

Qy       4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1517 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 1576

Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1577 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 1636

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1637 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 1696

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1697 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 1756

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1757 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 1816

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1817 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 1876

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1877 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 1936

Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1937 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 1996

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1997 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 2056

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2057 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 2116

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2117 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 2176

Qy       5350 TTTTCCCAGTCACGAC 5365
             ||||||||||||||||
Db       2177 TTTTCCCAGTCACGAC 2192
```

RESULT 13
ABQ78293
ID ABQ78293 standard; DNA; 3534 BP.
XX
AC ABQ78293;
XX
DT 05-NOV-2002 (first entry)
XX
DE Nucleotide sequence of vector pSPc5-12-HV-GHRH.
XX
KW Pig; growth hormone releasing hormone; GHRH; growth rate; lean body mass;
KW Insulin-like Growth Factor-I; IGF-I; milk production; feed efficiency;
KW somatotroph; growth-related disorder; hypopituitary dwarfism;
KW meat production; egg production; ss.
XX
OS Synthetic.
XX
PN WO200261037-A2.
XX
PD 08-AUG-2002.
XX
PF 12-DEC-2001; 2001WO-US048726.
XX
PR 12-DEC-2000; 2000US-0255021P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (ADVI-) ADVISYS.
XX
PI Schwartz RJ, Carpenter RH, Draghia-Akli R, Kern DR, Smith RG;
XX
DR WPI; 2002-619237/66.
XX
PT Improving or enhancing growth, lean body mass, milk production, feed
PT efficiency or Insulin-like Growth Factor-I levels, comprises introducing
PT a vector encoding a growth hormone releasing hormone into an animal
PT before or during gestation.
XX
PS Example 2; Page 109-111; 113pp; English.
XX
CC The present sequence represents vector pSPc5-12-HV-GHRH, which carries
CC cDNA encoding pig growth hormone releasing hormone (GHRH) cDNA. Nucleic
CC acids encoding GHRH are used in the method of the invention. The
CC specification describes a method for improving or enhancing
CC characteristics e.g. growth, lean body mass, Insulin-like Growth Factor
CC (IGF)-I levels, growth rate and milk production in an offspring, and for
CC delaying birth of an offspring. The method comprises introducing a
CC vector, encoding GHRH, into cells of the female animal prior to or during
CC gestation of the offspring under conditions where the nucleotide sequence
CC is expressed. The method is useful of improving or enhancing animal
CC growth, for increasing growth hormone, lean body mass, IGF-I levels, feed
CC efficiency, growth rate, ratio of somatotrophs to other hormone-producing
CC cells in a pituitary gland, and milk production in an offspring, and for
CC delaying birth of an offspring. GHRH nucleic acids and vectors are used
CC for diagnostic purposes in clinical medicine, both human and veterinary,
CC e.g. in treating growth-related disorders such as hypopituitary dwarfism
CC resulting from abnormalities in growth hormone production, and in
CC stimulating the growth and enhancing feed conversion efficiency of
CC animals raised for meat, milk and egg production
XX
SQ Sequence 3534 BP; 764 A; 1018 C; 979 G; 773 T; 0 U; 0 Other;

Query Match 39.8%; Score 2160; DB 6; Length 3534;
Best Local Similarity 99.5%; Pred. No. 1e-268;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             |||   |||  |     ||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1478

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1598

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1658

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
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Db      1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718
Qy      3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
Db      1719 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1778
Qy      3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
Db      1779 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1838
Qy      3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
Db      1839 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1898
Qy      3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
Db      1899 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1958
Qy      3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
Db      1959 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018
Qy      3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
Db      2019 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 2078
Qy      3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
Db      2079 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 2138
Qy      3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
Db      2139 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2198
Qy      4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
Db      2199 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2258
Qy      4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
Db      2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318
Qy      4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
Db      2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378
Qy      4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
Db      2379 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2438
Qy      4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
Db      2439 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2498
Qy      4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
Db      2499 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2558
Qy      4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
Db      2559 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2618
Qy      4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
Db      2619 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2678
Qy      4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
Db      2679 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2738
Qy      4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
Db      2739 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2798
Qy      4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
Db      2799 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2858
Qy      4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
Db      2859 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2918
Qy      4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
Db      2919 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2978
Qy      4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
Db      2979 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 3038
Qy      4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
Db      3039 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3098
Qy      4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
Db      3099 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 3158
Qy      4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
Db      3159 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3218
Qy      5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
Db      3219 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 3278
Qy      5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
Db      3279 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3338
Qy      5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
Db      3339 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3398
Qy      5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
Db      3399 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3458
Qy      5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
Db      3459 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3518
Qy      5350 TTTTCCCAGTCACGAC 5365
Db      3519 TTTTCCCAGTCACGAC 3534
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RESULT 14
AAL62060
ID AAL62060 standard; DNA; 3534 BP.
XX
AC AAL62060;
XX
DT 22-SEP-2003 (first entry)
XX
DE TV-GHRH plasmid DNA.
XX
KW Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;
KW sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;
KW lymphoma; weight loss; lymphopoesis; appetite stimulant; anoretic;
KW growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.
XX
OS Unidentified.
XX
PN WO2003049700-A2.

XX
PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-US039509.
XX
PR 11-DEC-2001; 2001US-0339610P.
XX
PA (ADVI-) ADVISYS INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;
PI Hahn K, Brenner MK;
XX
DR WPI; 2003-558968/52.
XX
PT Treating anemia, immune dysfunction, tumor, increasing total red blood
PT cell mass, reversing wasting or abnormal weight loss in subject, by
PT administering nucleic acid construct encoding growth-hormone-releasing-
PT hormone.
XX
PS Claim 4; Page 193-195; 212pp; English.
XX
CC The invention relates to compositions and methods for plasmid-mediated
CC supplementation. The method is useful for treating anaemia, tumour (such
CC as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
CC dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
CC kidney failure, for preventing the development of metastatic tumour, for
CC increasing total red blood cell mass, for reversing wasting, abnormal
CC weight loss or suppression of lymphopoesis, in a subject, or for
CC increasing weight gain in a chronically ill subject or, or for extending
CC life expectancy for a chronically ill subject. The present sequence is TV
CC -growth hormone releasing hormone (GHRH) plasmid DNA. This sequence is
CC used to illustrate the method of the invention
XX
SQ Sequence 3534 BP; 764 A; 1016 C; 979 G; 775 T; 0 U; 0 Other;

Query Match 39.8%; Score 2160; DB 9; Length 3534;
Best Local Similarity 99.5%; Pred. No. 1e-268;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy      3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
             |||   |||  |    ||||||||||||||||||||||||||||||||||||||||||||
Db      1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy      3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1419 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1478

Qy      3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy      3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1539 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1598

Qy      3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1599 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1658

Qy      3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718

Qy      3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1719 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1778

Qy      3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1779 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1838

Qy      3670 CTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1839 CTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1898

Qy      3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1899 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 1958

Qy      3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1959 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018

Qy      3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2019 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 2078

Qy      3910 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2079 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 2138

Qy      3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2139 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2198

Qy      4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2199 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2258

Qy      4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318

Qy      4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378

Qy      4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2379 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2438

Qy      4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2439 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2498

Qy      4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2499 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2558

Qy      4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2559 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2618

Qy      4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2619 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2678

Qy      4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2679 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2738

Qy      4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2739 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2798

Qy      4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2799 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 2858

Qy      4690 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2859 GTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCG 2918

Qy      4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2919 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 2978

Qy       4810 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 4869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2979 TCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCC 3038

Qy       4870 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 4929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3039 AGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTC 3098

Qy       4930 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 4989
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3099 TTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAG 3158

Qy       4990 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 5049
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3159 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3218

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
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Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
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Db       3279 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3338

Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
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Db       3339 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3398

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
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Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3459 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3518

Qy       5350 TTTTCCCAGTCACGAC 5365
              ||||||||||||||||
Db       3519 TTTTCCCAGTCACGAC 3534
```

RESULT 15
AAL62062
ID AAL62062 standard; DNA; 3534 BP.
XX
AC AAL62062;
XX
DT 22-SEP-2003 (first entry)
XX
DE Wild-type GHRH plasmid DNA, pSP-wt-GHRH.
XX
KW Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;
KW sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;
KW lymphoma; weight loss; lymphopoesis; appetite stimulant; anoretic;
KW growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.
XX
OS Unidentified.
XX
PN WO2003049700-A2.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-US039509.
XX
PR 11-DEC-2001; 2001US-0339610P.
XX
PA (ADVI-) ADVISYS INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;
PI Hahn K, Brenner MK;
XX
DR WPI; 2003-558968/52.
XX
PT Treating anemia, immune dysfunction, tumor, increasing total red blood
PT cell mass, reversing wasting or abnormal weight loss in subject, by
PT administering nucleic acid construct encoding growth-hormone-releasing-
PT hormone.
XX
PS Example 1; Page 198-200; 212pp; English.
XX
CC The invention relates to compositions and methods for plasmid-mediated
CC supplementation. The method is useful for treating anaemia, tumour (such
CC as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
CC dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
CC kidney failure, for preventing the development of metastatic tumour, for
CC increasing total red blood cell mass, for reversing wasting, abnormal
CC weight loss or suppression of lymphopoesis, in a subject, or for
CC increasing weight gain in a chronically ill subject or, or for extending
CC life expectancy for a chronically ill subject. The present sequence is
CC wild-type growth hormone releasing hormone (GHRH) plasmid DNA. This
CC sequence is used to illustrate the method of the invention
XX
SQ Sequence 3534 BP; 764 A; 1015 C; 981 G; 774 T; 0 U; 0 Other;

  Query Match   39.8%; Score 2160; DB 9; Length 3534;
  Best Local Similarity   99.5%; Pred. No. 1e-268;
  Matches 2166; Conservative   0; Mismatches   10; Indels   0; Gaps   0;

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Qy       3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 3249
              |||   |||  |     ||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCG 1418

Qy       3250 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 3309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 TAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC 1478

Qy       3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 3369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA 1538

Qy       3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT 1598

Qy       3430 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 3489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCC 1658

Qy       3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1659 TCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718

Qy       3550 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1719 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 1778

Qy       3610 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1779 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 1838

Qy       3670 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1839 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1898

Qy       3730 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3790 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
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Db       1959 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018

Qy       3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3909
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Db       2019 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 2078

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Db       2079 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 2138

Qy       3970 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4029
Db       2139 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 2198

Qy       4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4089
Db       2199 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 2258

Qy       4090 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 4149
Db       2259 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA 2318

Qy       4150 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 4209
Db       2319 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT 2378

Qy       4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269
Db       2379 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 2438

Qy       4270 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 4329
Db       2439 ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAA 2498

Qy       4330 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 4389
Db       2499 TCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCT 2558

Qy       4390 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 4449
Db       2559 TCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGG 2618

Qy       4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 4509
Db       2619 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCA 2678

Qy       4510 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 4569
Db       2679 TCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAAC 2738

Qy       4570 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 4629
Db       2739 AGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCG 2798

Qy       4630 GCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAG 4689
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Qy       4750 GCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAG 4809
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Db       3159 CCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAA 3218

Qy       5050 CCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCA 5109
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Qy       5110 GATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
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Qy       5170 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 5229
Db       3339 CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC 3398

Qy       5230 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 5289
Db       3399 CATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA 3458

Qy       5290 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 5349
Db       3459 TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGG 3518

Qy       5350 TTTTCCCAGTCACGAC 5365
Db       3519 TTTTCCCAGTCACGAC 3534
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Search completed: February 20, 2006, 19:34:42
Job time : 2802 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 18:57:52 ; Search time 19467 Seconds
(without alignments)
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Title: US-10-798-896-1
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Sequence: 1 ccaccgcggtggcggccgtc.....ctatagggcgaattggagct 5423

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1006.8	18.6	1186	8	DR045845	DR045845 FP-10_F08
2	992.4	18.3	1176	8	CX943193	CX943193 LamjGestG
3	987.2	18.2	1067	1	AU081137	AU081137 AU081137
4	959	17.7	1089	1	AU081124	AU081124 AU081124
5	903.2	16.7	1049	10	CL021189	CL021189 CH216-8A1
c 6	901	16.6	925	6	CB686151	CB686151 Bn01b_02o
7	893.2	16.5	1191	8	DR045882	DR045882 FP-11_A09
8	859.2	15.8	885	10	CL076016	CL076016 CH216-138
9	853	15.7	1195	8	DR046031	DR046031 FP-8_F02.
10	852.8	15.7	951	8	CV983341	CV983341 UMC-bof_0
11	852.6	15.7	875	8	CX012952	CX012952 io62d12.b
12	835.6	15.4	1073	6	CF269652	CF269652 Fcylcold8
13	824.4	15.2	1169	10	AG332951	AG332951 Mus muscu
14	823.2	15.2	1025	10	CL021193	CL021193 CH216-8A1
15	820.4	15.1	1163	1	AU081044	AU081044 AU081044
16	818.8	15.1	868	8	CV984340	CV984340 UMC-bov_0
c 17	812.6	15.0	935	7	CK284786	EST747508
c 18	804.8	14.8	833	6	CB686421	CB686421 Bn01b_04j
19	803.6	14.8	966	9	BZ570738	BZ570738 msh2_1513
20	800.4	14.8	804	8	CV979032	CV979032 UMC-bemiv
21	798.6	14.7	813	8	CX006605	CX006605 io23f10.b
c 22	796	14.7	804	7	CK291519	CK291519 EST754233
c 23	796	14.7	856	7	CK287297	CK287297 EST750019
c 24	796	14.7	910	7	CK287930	CK287930 EST750652
c 25	796	14.7	933	7	CK291799	CK291799 EST754513
c 26	796	14.7	936	7	CK256977	CK256977 EST740614
c 27	796	14.7	947	7	CK298208	CK298208 EST760922
c 28	796	14.7	954	7	CK283361	CK283361 EST746083
c 29	794	14.6	811	7	CK288185	CK288185 EST750907
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31	786.2	14.5	865	7	CK125894	CK125894 BES182411
32	783.4	14.4	833	8	CX013029	CX013029 io62h07.b
33	779.4	14.4	846	7	CV468077	CV468077 est_l_van
34	779	14.4	841	8	CX011012	CX011012 io49h10.b
35	778.8	14.4	894	8	DN641029	DN641029 UMC-bend_
36	777.6	14.3	1164	8	DR045996	DR045996 FP-8_C03.
37	775.8	14.3	1194	9	BZ578985	BZ578985 msh2_6095
38	774	14.3	954	1	AL044364	AL044364 DKFZp434C
39	773.4	14.3	776	8	CX006479	CX006479 io23a02.b
40	772.2	14.2	808	8	CX006965	CX006965 io25f10.b
41	769.2	14.2	863	6	CF752100	CF752100 TGDR9 Hum
42	762.2	14.1	814	8	CX008423	CX008423 io34d12.b
43	762	14.1	1249	9	BZ572284	BZ572284 msh2_2572
44	761.4	14.0	959	9	BZ557985	BZ557985 pacs1-60_
45	761	14.0	761	8	CX008002	CX008002 io31f11.b

ALIGNMENTS

RESULT 1
DR045845
LOCUS DR045845 1186 bp mRNA linear EST 02-JUN-2005
DEFINITION FP-10_F08.SEQ cDNA library of Phaeosphaeria nodorum grown on wheat cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.
ACCESSION DR045845
VERSION DR045845.1 GI:66909681
KEYWORDS EST.
SOURCE Phaeosphaeria nodorum
ORGANISM Phaeosphaeria nodorum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
REFERENCE 1 (bases 1 to 1186)
AUTHORS Bindschedler,L.V., Cooper,R.M., Thomas,S.W., Madrid,M.P. and Oliver,R.P.
TITLE cDNA library of Phaeosphaeria nodorum grown on Wheat cell walls
JOURNAL Unpublished (2005)
COMMENT Contact: Richard Oliver
Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
Murdoch University
South Street, Murdoch, W.A 6150, Australia
Tel: +0893607404
Email: roliver@murdoch.edu.au.
FEATURES Location/Qualifiers
source 1. .1186
/organism="Phaeosphaeria nodorum"
/mol_type="mRNA"
/db_xref="taxon:13684"
/clone_lib="cDNA library of Phaeosphaeria nodorum grown on wheat cell walls"
ORIGIN

Query Match 18.6%; Score 1006.8; DB 8; Length 1186;
Best Local Similarity 98.2%; Pred. No. 1.6e-276;
Matches 1039; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

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Qy       3248 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA 3307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA 82

Qy       3308 ACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA 3367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA 142

Qy       3368 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 3427
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Db        143 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 202

Qy       3428 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 3487
Db        203 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 262

Qy       3488 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACT 3547
Db        263 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACT 322

Qy       3548 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG 3607
Db        323 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG 382

Qy       3608 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 3667
Db        383 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 442

Qy       3668 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 3727
Db        443 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 502

Qy       3728 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 3787
Db        503 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 562

Qy       3788 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 3847
Db        563 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 622

Qy       3848 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 3907
Db        623 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 682

Qy       3908 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 3967
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Qy       3968 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 4027
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Qy       4028 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 4087
Db        803 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 862

Qy       4088 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 4147
Db        863 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 922

Qy       4148 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 4207
Db        923 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 982

Qy       4208 TTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTT 4267
Db        983 TTTGCAAGCAGCAGA-TACGCGCAGAAAAAAATGATCTCAAGAAGAT-CTTTGATCTTTT 1040

Qy       4268 CTACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGG 4305
Db       1041 TCTACGGGTCTGACGCTCAGTGACGAAACTCACGTAGG 1078


RESULT 2
CX943193
LOCUS       CX943193               1176 bp    mRNA    linear   EST 09-FEB-2005
DEFINITION  LamjGestGS8 Laminaria japonica Lambda Zap Express Library Laminaria
            japonica cDNA 5', mRNA sequence.
ACCESSION   CX943193
VERSION     CX943193.1  GI:58802440
KEYWORDS    EST.
SOURCE      Laminaria japonica
  ORGANISM  Laminaria japonica
            Eukaryota; stramenopiles; Phaeophyceae; Laminariales;
            Laminariaceae; Laminaria.
REFERENCE   1  (bases 1 to 1176)
  AUTHORS   Xuan,J., Zhao,G., Wang,W., Duan,D., Weng,M. and Wang,B.
  TITLE     Expressed sequence tag analysis of the brown alga Laminaria
            japonica (Phaeophyceae)
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Xuan JS
            The State Key Laboratory of Plant Genome Research
            Institute of Genetics and Developmental Biology, Chinese Academy of
            Science
            Datun Road, Chaoyang District, Beijing, China, 100101
            Tel: 086 010 64889353
            Fax: 086 010 64873428
            Email: bnuxuan@hotmail.com
            Seq primer: T3 Forward
            High quality sequence stop: 1176.
FEATURES             Location/Qualifiers
     source          1. .1176
                     /organism="Laminaria japonica"
                     /mol_type="mRNA"
                     /db_xref="taxon:88149"
                     /sex="female"
                     /dev_stage="gametophyte"
                     /clone_lib="Laminaria japonica Lambda Zap Express Library"
                     /note="Vector: Uni-ZAP@ XR vector; Site_1: EcoRI; Site_2:
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ORIGIN

  Query Match             18.3%;  Score 992.4;  DB 8;  Length 1176;
  Best Local Similarity   99.0%;  Pred. No. 2.2e-272;
  Matches 1030;  Conservative    0;  Mismatches    6;  Indels    4;  Gaps    3;

Qy       3248 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA 3307
Db          37 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA 96

Qy       3308 ACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA 3367
Db          97 ACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA 156

Qy       3368 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 3427
Db         157 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 216

Qy       3428 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 3487
Db         217 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 276

Qy       3488 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACT 3547
Db         277 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACT 336

Qy       3548 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG 3607
Db         337 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG 396

Qy       3608 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 3667
Db         397 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 456

Qy       3668 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 3727
Db         457 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 516

Qy       3728 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 3787
Db         517 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 576

Qy       3788 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 3847
Db         577 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 636
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Qy       3848 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 3907
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Db        637 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 696

Qy       3908 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 3967
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 756

Qy       3968 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 4027
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Db        757 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 816

Qy       4028 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 4087
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Db        817 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 876

Qy       4088 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 4147
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Db        877 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 936

Qy       4148 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 4207
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Db        937 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGG-TTTTTTG 995

Qy       4208 TTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTT 4267
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Db        996 TTTGCAAGCAGCAGATTACGCGCAGAAAAAA--GGATCTCAGAAGATCCTTTGATCTTTT 1053

Qy       4268 CTACGGGGTCTGACGCTCAG 4287
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Db       1054 CTAC-GGGTCTGACGCTCAG 1072
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RESULT 3
AU081137
LOCUS       AU081137                1067 bp    mRNA    linear   EST 30-JUL-2002
DEFINITION  AU081137 Oncorhynchus mykiss Kidney infected by infectious
            hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KI2,
            mRNA sequence.
ACCESSION   AU081137
VERSION     AU081137.1  GI:6431485
KEYWORDS    EST.
SOURCE      Oncorhynchus mykiss (rainbow trout)
  ORGANISM  Oncorhynchus mykiss
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE   1  (bases 1 to 1067)
  AUTHORS   Kono,T., Sakai,M. and LaPatra,S.E.
  TITLE     Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
            Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
            Hematopoietic Necrosis Virus
  JOURNAL   Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT     Contact: Masahiro Sakai
            Faculty of Agriculture
            Miyazaki University
            1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
            Email: m.sakai@cc.miyazaki-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .1067
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                     /mol_type="mRNA"
                     /db_xref="taxon:8022"
                     /clone="KI2"
                     /tissue_type="kidney"
                     /clone_lib="Oncorhynchus mykiss Kidney infected by
                     infectious hematopoietic necrosis virus"
                     /note="common name:rainbow trout ; infected by infectious
                     hematopoietic necrosis virus"
ORIGIN

  Query Match             18.2%;  Score 987.2;  DB 1;  Length 1067;
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  Best Local Similarity   99.0%;  Pred. No. 6.6e-271;
  Matches 1014;  Conservative    0;  Mismatches    8;  Indels    2;  Gaps    2;

Qy       3207 CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCT 3266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         46 CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCT 105

Qy       3267 GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT 3326
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT 165

Qy       3327 AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC 3386
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC 225

Qy       3387 ACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG 3446
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG 285

Qy       3447 CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT 3506
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT 345

Qy       3507 GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT 3566
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Db        346 GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT 405

Qy       3567 ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGC 3626
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Db        406 ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGC 465

Qy       3627 CAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGA 3686
             ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        466 CAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTVVTTCCATAGGCTCCGCCCCCCTGACGA 525

Qy       3687 GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA 3746
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA 585

Qy       3747 CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC 3806
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC 645

Qy       3807 CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG 3866
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Db        646 CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG 705

Qy       3867 TAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC 3926
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Db        706 TAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC 765

Qy       3927 CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG 3986
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG 825

Qy       3987 ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGT 4046
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Db        826 ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGT 885

Qy       4047 AGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGT 4106
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Db        886 AGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGT 945

Qy       4107 ATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTG 4166
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 ATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTG 1005

Qy       4167 ATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTAC 4226
             ||||||||||||||  || ||||||||||||     |||||||||||||| ||||||||||||
Db       1006 ATCCGGCAAACAAA-CAACGCTGGTAGCGTGTTTTTTTTTGTTTGC-AGCAGCAGATTAC 1063

Qy       4227 GCGC 4230
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Db       1064 GCGC 1067


RESULT 4
AU081124
LOCUS       AU081124               1089 bp    mRNA    linear   EST 30-JUL-2002
DEFINITION  AU081124 Oncorhynchus mykiss Kidney infected by infectious
            hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KG'12,
            mRNA sequence.
ACCESSION   AU081124
VERSION     AU081124.1  GI:6431472
KEYWORDS    EST.
SOURCE      Oncorhynchus mykiss (rainbow trout)
  ORGANISM  Oncorhynchus mykiss
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE   1  (bases 1 to 1089)
  AUTHORS   Kono,T., Sakai,M. and LaPatra,S.E.
  TITLE     Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
            Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
            Hematopoietic Necrosis Virus
  JOURNAL   Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT     Contact: Masahiro Sakai
            Faculty of Agriculture
            Miyazaki University
            1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
            Email: m.sakai@cc.miyazaki-u.ac.jp.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:8022"
                     /clone="KG'12"
                     /tissue_type="kidney"
                     /clone_lib="Oncorhynchus mykiss Kidney infected by
                     infectious hematopoietic necrosis virus"
                     /note="common name:rainbow trout ; infected by infectious
                     hematopoietic necrosis virus"
ORIGIN

  Query Match             17.7%;  Score 959;  DB 1;  Length 1089;
  Best Local Similarity   97.5%;  Pred. No. 8.2e-263;
  Matches 1017;  Conservative    0;  Mismatches   20;  Indels    6;  Gaps    4;

Qy       3207 CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCT 3266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         47 CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCT 106

Qy       3267 GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT 3326
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Db        107 GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT 166

Qy       3327 AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC 3386
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC 226

Qy       3387 ACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG 3446
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG 286

Qy       3447 CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT 3506
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Db        287 CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT 346

Qy       3507 GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT 3566
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Db        347 GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT 406

Qy       3567 ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGC 3626
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGC 466

Qy       3627 CAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGA 3686
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Db        467 CAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGA 526

Qy       3687 GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA 3746
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA 586

Qy       3747 CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC 3806
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Db        587 CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC 646

Qy       3807 CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG 3866
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Qy       3867 TAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC 3926
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Qy       3927 CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG 3986
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Db        767 CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG 826

Qy       3987 ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGT 4046
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Qy       4047 AGGCGGTGCTACAGAGTTCTTGAAG-TGGTGGCCTAACTACGGCTACACTAGAAGAACAG 4105
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Db        887 AGGCGGTGCTACAGAGTTCTTGAAGTTTGTGGCCTAACTACGGCTACACTAGAAGAACAG 946

Qy       4106 TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTT 4165
             ||||| |||||||||||||||| |||||||||||||||||||||||| ||||||||||||
Db        947 TATTTTGTATCTGCGCTCTGCTGGAGCCAGTTACCTTCGGAAAAAGAGTGGGTAGCTCTT 1006

Qy       4166 -GATCCGGCAAACAAACCA---CCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA-GCA 4220
              |||||||||||||||| ||    |   |   | ||  || ||||||||||||||| ||| |||
Db       1007 GGATCCGGCAAACAAAACAACCGCTGGGAAGGGGGGTGTCTTTTTGTTTGCAAGCACGCA 1066

Qy       4221 GATTACGCGCAGAAAAAAAGGAT 4243
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Db       1067 GATTACCCGCGAAAAAAACGGAT 1089


RESULT 5
CL021189
LOCUS       CL021189               1049 bp    DNA     linear   GSS 31-DEC-2003
DEFINITION  CH216-8A14_RM1.1 CH216 Xenopus tropicalis genomic clone CH216-8A14,
            genomic survey sequence.
ACCESSION   CL021189
VERSION     CL021189.1  GI:40463002
KEYWORDS    GSS.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 1049)
  AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
            Mardis,E. and Wilson,R.
  TITLE     A physical map of the xenopus tropicalis genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 175000   Std Error: 0.00
            Seq primer: RM1 TACGACTCACTATAGGGAGA
            Class: BAC ends
            High quality sequence start: 43
            High quality sequence stop: 888.
FEATURES             Location/Qualifiers
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                     /clone="CH216-8A14"
                     /sex="male"
                     /cell_line="Stock 248 F7A2, inbred N7"
                     /clone_lib="CH216"
                     /note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                     BAC library"
ORIGIN

  Query Match             16.7%;  Score 903.2;  DB 10;  Length 1049;
  Best Local Similarity   98.4%;  Pred. No. 8.5e-247;
  Matches  933;  Conservative    0;  Mismatches   13;  Indels    2;  Gaps    2;

Qy       3237 TTCGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC 3296
             | | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 TGCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC 160

Qy       3297 AATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGT 3356
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Db        161 AATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGT 220

Qy       3357 GAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTC 3416
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Db        221 GAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTC 280

Qy       3417 GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCG 3476
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCG 340

Qy       3477 CTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGT 3536
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 CTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGT 400

Qy       3537 ATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAA 3596
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 ATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAA 460

Qy       3597 GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGC 3656
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGC 520

Qy       3657 GTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAG 3716
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 GTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAG 580

Qy       3717 GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGT 3776
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGT 640

Qy       3777 GCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGG 3836
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 GCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGG 700

Qy       3837 AAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCG 3896
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 AAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCG 760

Qy       3897 CTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGG 3956
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 CTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGG 820

Qy       3957 TAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCAC 4016
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 TAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCAC 880

Qy       4017 TGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTG 4076
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        881 TGGTAACAGGATTAGCAGAGCGAGGTATGTAAGCGGTGCTACAGAGTTCTTGAAGTGGTG 940

Qy       4077 GCCTAACTACGGCTACACTAGAAGAAC-AGTATTTGGTATCTGCGCTCTGCTGAAGCCAG 4135
             |||||||||||||||||||||||||||| |||||||| |||||||||||||||||| ||||
Db        941 GCCTAACTACGGCTACACTAGAAGAACAAGTATTTGTTATCTGCGCTCTGCTGAAACCAG 1000

Qy       4136 TTACC-TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACC 4182
             ||||| |||||||||| |||||||||||||||  | |  || ||| |
Db       1001 TTACCTTTCGGAAAAAAAGTTGGTAGCTCTTGAATCCGGCAAAAAAAC 1048


RESULT 6
CB686151/c
LOCUS       CB686151                925 bp    mRNA    linear   EST 09-APR-2003
DEFINITION  Bn01b_02o08_A
            Bn01b_AAFC_ECORC_transgenic_Brassica_napus_overexpressing_BNCBF17_c
            onstitutively_frost_tolerant Brassica napus cDNA clone Bn01b_02o08,
            mRNA sequence.
ACCESSION   CB686151
VERSION     CB686151.1  GI:29689876
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 925)
  AUTHORS   Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A.,
            Chagnon,J., Farah,S., Couroux,P. and Hattori,J.
  TITLE     Expressed Sequence Tags from constitutively frost tolerant
            transgenic Brassica napus overexpressing BNCBF17
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Singh,J.A.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
            0C6, Canada
            Tel: (613) 759-1662
            Fax: (613) 759-1701
            Email: singhja@agr.gc.ca.
FEATURES             Location/Qualifiers
     source          1. .925
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Westar"
                     /db_xref="taxon:3708"
                     /clone="Bn01b_02o08"
                     /tissue_type="fourth leaf"
                     /dev_stage="3 weeks seedling grown at room temperature"
                     /clone_lib="Bn01b_AAFC_ECORC_transgenic_Brassica_napus_ove
                     rexpressing_BNCBF17_constitutively_frost_tolerant"
                     /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;
                     Site_2: XhoI; Germinated in soil flats and seedlings grown
                     for 3 weeks in a Conviron E-15 cabinet set at 20oC /16 hr
                     light (250 Em-2sec-1) and 16 oC / 8 hr dark. Fourth leaves
                     collected at 9 am and immediately frozen."
ORIGIN

  Query Match             16.6%;  Score 901;  DB 6;  Length 925;
  Best Local Similarity   98.6%;  Pred. No. 3.5e-246;
  Matches  912;  Conservative    6;  Mismatches    6;  Indels    1;  Gaps    1;

Qy       3212 TTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCTGTTTC 3271
             |||  | |||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db        924 TTTTGTTCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTT- 866

Qy       3272 CTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGT 3331
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 CTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGT 806

Qy       3332 GTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGC 3391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 GTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGC 746

Qy       3392 CCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGG 3451
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Db        745 CCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGG 686

Qy       3452 GGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCT 3511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 GGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCT 626

Qy       3512 CGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA 3571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 CGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA 566

Qy       3572 CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGA 3631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGA 506

Qy       3632 ACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATC 3691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 ACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATC 446

Qy       3692 ACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG 3751
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 ACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG 386

Qy       3752 CGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGAT 3811
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGAT 326

Qy       3812 ACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGT 3871
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 ACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGT 266

Qy       3872 ATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTC 3931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 ATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTC 206

Qy       3932 AGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACG 3991
             |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 AGCCCGASCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACG 146

Qy       3992 ACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCG 4051
             ||||||||||||||:|||||||||||||||:|||||:||||||||||||||||||||||||
Db        145 ACTTATCGCCACTGGSAGCAGCCACTGGTAACARGATTASCAGAGCGAGGTATGTAGGCG 86

Qy       4052 GTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTG 4111
             ||||||||||||||:|||||||||| |||||||||:||||||||||||||||||||||||||
Db          85 GTGCTACAGAGTTCTTSAAGTGGTGGCTTAACTACGGSTACACTAGAAGAACAGTATTTG 26

Qy       4112 GTATCTGCGCTCTGCTGAAGCCAGT 4136
             |||||||||||||||||||||||||
Db          25 GTATCTGCGCTCTGCTGAAGCCAGT 1
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RESULT 7
DR045882
LOCUS       DR045882               1191 bp    mRNA    linear   EST 02-JUN-2005
DEFINITION  FP-11_A09.SEQ cDNA library of Phaeosphaeria nodorum grown on wheat
            cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.
ACCESSION   DR045882
VERSION     DR045882.1  GI:66909718
KEYWORDS    EST.
SOURCE      Phaeosphaeria nodorum
  ORGANISM  Phaeosphaeria nodorum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
            Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
REFERENCE   1  (bases 1 to 1191)
  AUTHORS   Bindschedler,L.V., Cooper,R.M., Thomas,S.W., Madrid,M.P. and
            Oliver,R.P.
  TITLE     cDNA library of Phaeosphaeria nodorum grown on Wheat cell walls
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Richard Oliver
            Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
            Murdoch University
            South Street, Murdoch, W.A 6150, Australia
            Tel: +0893607404
            Email: roliver@murdoch.edu.au.
FEATURES             Location/Qualifiers
     source          1. .1191
                     /organism="Phaeosphaeria nodorum"
                     /mol_type="mRNA"
                     /db_xref="taxon:13684"
                     /clone_lib="cDNA library of Phaeosphaeria nodorum grown on
                     wheat cell walls"
ORIGIN
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  Query Match             16.5%;  Score 893.2;  DB 8;  Length 1191;
  Best Local Similarity   99.2%;  Pred. No. 6.6e-244;
  Matches  919;  Conservative    0;  Mismatches    3;  Indels    4;  Gaps    2;

Qy       3207 CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCT 3266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCT 173

Qy       3267 GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT 3326
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT 233

Qy       3327 AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC 3386
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC 293

Qy       3387 ACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG 3446
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG 353

Qy       3447 CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT 3506
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT 413

Qy       3507 GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT 3566
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT 473

Qy       3567 ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGC 3626
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGC 533

Qy       3627 CAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGA 3686
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 CAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGA 593

Qy       3687 GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA 3746
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA 653

Qy       3747 CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC 3806
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC 713

Qy       3807 CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG 3866
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG 773

Qy       3867 TAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC 3926
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 TAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC 833

Qy       3927 CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG 3986
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG 893

Qy       3987 ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGT 4046
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGT 953

Qy       4047 AGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGT 4106
                |  ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||
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Db        954 CG--CGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGA--GACAGT 1009

Qy       4107 ATTTGGTATCTGCGCTCTGCTGAAGC 4132
              ||||||||||||||||||||||||||
Db       1010 ATTTGGTATCTGCGCTCTGCTGAAGC 1035


RESULT 8
CL076016
LOCUS       CL076016                885 bp    DNA     linear   GSS 31-DEC-2003
DEFINITION  CH216-138F20_RM1.1 CH216 Xenopus tropicalis genomic clone
            CH216-138F20, genomic survey sequence.
ACCESSION   CL076016
VERSION     CL076016.1  GI:40531929
KEYWORDS    GSS.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 885)
  AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
            Mardis,E. and Wilson,R.
  TITLE     A physical map of the xenopus tropicalis genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 175000   Std Error: 0.00
            Seq primer: RM1 TACGACTCACTATAGGGAGA
            Class: BAC ends
            High quality sequence start: 11
            High quality sequence stop: 810.
FEATURES             Location/Qualifiers
     source          1. .885
                     /organism="Xenopus tropicalis"
                     /mol_type="genomic DNA"
                     /strain="Nigerian frog"
                     /db_xref="taxon:8364"
                     /clone="CH216-138F20"
                     /sex="male"
                     /cell_line="Stock 248 F7A2, inbred N7"
                     /clone_lib="CH216"
                     /note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                     BAC library"
ORIGIN

  Query Match            15.8%;  Score 859.2;  DB 10;  Length 885;
  Best Local Similarity   99.4%;  Pred. No. 3.4e-234;
  Matches  872;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       3280 AATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCC 3339
              ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 AATTTGTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCC 64

Qy       3340 TGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTC 3399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 TGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTC 124

Qy       3400 CAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGC 3459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGC 184

Qy       3460 GGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTT 3519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 GGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTT 244

Qy       3520 CGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCA 3579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCA 304

Qy       3580 GGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAA 3639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAA 364

Qy       3640 AAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAAT 3699
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 AAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAAT 424

Qy       3700 CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCC 3759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCC 484

Qy       3760 CCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCC 3819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCC 544

Qy       3820 GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT 3879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT 604

Qy       3880 TCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAC 3939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 TCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAC 664

Qy       3940 CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCG 3999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCG 724

Qy       4000 CCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA 4059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 CCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA 784

Qy       4060 GAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGC 4119
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        785 GAGTTCTTGAAGTGGTGGCCTAACTACNGCTACACTAGAAGAACAGTATTTGGTATCTGC 844

Qy       4120 GCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTG 4156
              |||||||||||| |||||||||||||||||||||| |
Db        845 GCTCTGCTGAAG-CAGTTACCTTCGGAAAAAGAGTGG 880


RESULT 9
DR046031
LOCUS       DR046031                1195 bp    mRNA    linear   EST 02-JUN-2005
DEFINITION  FP-8_F02.SEQ cDNA library of Phaeosphaeria nodorum grown on wheat
            cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.
ACCESSION   DR046031
VERSION     DR046031.1  GI:66909867
KEYWORDS    EST.
SOURCE      Phaeosphaeria nodorum
  ORGANISM  Phaeosphaeria nodorum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
            Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Bindschedler,L.V., Cooper,R.M., Thomas,S.W., Madrid,M.P. and
            Oliver,R.P.
  TITLE     cDNA library of Phaeosphaeria nodorum grown on Wheat cell walls
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Richard Oliver
            Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
            Murdoch University
            South Street, Murdoch, W.A 6150, Australia
            Tel: +0893607404
            Email: roliver@murdoch.edu.au.
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Phaeosphaeria nodorum"
                     /mol_type="mRNA"
                     /db_xref="taxon:13684"
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                     wheat cell walls"
ORIGIN

  Query Match            15.7%;  Score 853;  DB 8;  Length 1195;
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  Best Local Similarity   98.2%;  Pred. No. 2.3e-232;
  Matches  906;  Conservative    0;  Mismatches   10;  Indels    7;  Gaps    4;

Qy       3207 CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCT 3266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCT 228

Qy       3267 GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT 3326
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Db        229 GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT 288

Qy       3327 AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC 3386
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Db        289 AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC 348

Qy       3387 ACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG 3446
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Db        349 ACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG 408

Qy       3447 CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT 3506
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT 468

Qy       3507 GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT 3566
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3567 ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGC 3626
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Qy       3627 CAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGA 3686
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Qy       3687 GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA 3746
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Db        649 GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA 708

Qy       3747 CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC 3806
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Db        709 CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC 768

Qy       3807 CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG 3866
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Db        769 CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG 828

Qy       3867 TAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC 3926
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Qy       3927 CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG 3986
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Qy       3987 ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGT 4046
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Db        949 A-ACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGT 1007

Qy       4047 AGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGT 4106
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Db       1008 AG--CGTGCTACAGAGTTCTTGAAGTGGTGGCCTA---CTACGCTACCTAGAAGAACAGT 1062

Qy       4107 ATTTGGTATCTGCGCTCTGCTGA 4129
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Db       1063 A-TTGGTATCTGCGCTCTGCTGA 1084


RESULT 10
CV983341
LOCUS       CV983341                951 bp    mRNA    linear   EST 30-NOV-2004
DEFINITION  UMC-bof_0A01-002-g06 Ovarian Follicle bof Bos taurus cDNA 3', mRNA
            sequence.
ACCESSION   CV983341
VERSION     CV983341.1  GI:56144062
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 951)
  AUTHORS   Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C.,
            Roberts,R.M., Smith,M.F. and Youngquist,R.S.
  TITLE     USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
            Reproduction
  JOURNAL   Unpublished (2002)
COMMENT     Contact: DNA Core Facility (Bovine Project)
            Animal Science - RS Prather
            University of Missouri-Columbia
            M616 Medical Sciences Bldg., Columbia, MO 65212, USA
            Tel: (573)882-0428
            Fax: (573)884-5552
            Email: bovine@rnet.missouri.edu
            POLYA=No.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /dev_stage="Ovarian Follicle"
                     /clone_lib="bof"
                     /note="Vector: pSport1; Funding: The production of ESTs
                     submitted in this project was funded by USDA Grant
                     MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female
                     Reproduction' to RS Prather(Primary Investigator), E
                     Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF
                     Smith and RS Youngquist. Genetic Source: Heifers for the
                     project were purchased from Circle A Ranch, Iberia, MO
                     (http://www.circlearanch.com/home.html). These heifers,
                     while not registered have known Angus pedigrees going back
                     at least 4 generations. Samples collected: The samples
                     consisted of the following: germinal vesicle-stage
                     oocytes; in vitro derived embryos (2-cell, morula,
                     blastocyst and nuclear transfer blastocyst); in vivo
                     blastocysts and conceptuses (days 8, 14, 16 and 18);
                     corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian
                     follicles (days 0, non-recruited, recruited, early
                     selected and preovulatory); oviduct (days 0, 3 and 5);
                     endometrium (days 5, 8, 14, 16, 18 and 35); and
                     placenta/embryo from day 35 conceptuses. Expanded
                     descriptions of how the tissues were collected can be
                     found at the following URL:
                     http://genome.rnet.missouri.edu/Bovine/Methods.html.
                     Library construction (Standard Protocol): All procedures
                     have been described in detail elsewhere (Soares et al.,
                     1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
                     cellular RNA from each sample was isolated by using
                     STAT-60 reagent (Tel-Test, Friendswood, TX) and the
                     poly(A)+ RNA was obtained by two rounds of purification
                     with the Oligotex mRNA isolation kit (Qiagen) according to
                     the manufacturer's instructions. The libraries were
                     constructed essentially as described by the manufacturer's
                     instructions provided with the SuperScript Plasmid System
                     (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of
                     poly(A)+ RNA was annealed at c37 degrees with 10mcg of
                     NotI-tag-dT18 oligonucleotide (GCTGCTCGCGGCCGC-tag-T18)
                     and reverse transcribed at c37 degrees with SuperScript II
                     (Invitrogen) reverse transcriptase (Jiang et al., 2001).
                     The 'tag' represents a tissue/stage-specific ten-base
                     sequence identifier
                     (http://genome.uiowa.edu/pubsoft/software.html) present in
                     the oligonucleotide used to prime first-strand synthesis.
                     Second strand synthesis was performed with T4 DNA
                     polymerase in the presence of DNA ligase and RNase H.
                     After second strand synthesis, the double-stranded cDNAs
```

were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dT18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dT oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@rnet.missouri.edu. Bonaldo MF, Lennon G, Soares MB,. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.
TAG_TISSUE=Ovarian Follicle
TAG_SEQ=Not found"

ORIGIN

Query Match 15.7%; Score 852.8; DB 8; Length 951;
Best Local Similarity 99.8%; Pred. No. 2.4e-232;
Matches 854; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3498 TGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGT 3557
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Db         62 TGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGT 121

Qy       3558 AATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCA 3617
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Qy       3618 GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 3677
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Db        242 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 301

Qy       3738 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 3797
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Qy       3858 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 3917
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Db        422 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 481

Qy       3918 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 3977
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Db        482 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 541

Qy       3978 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 4037
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Qy       4038 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 4097
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Qy       4098 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 4157
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Db        662 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 721

Qy       4158 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 4217
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Db        722 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 781

Qy       4218 GCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC 4277
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Db        782 GCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC 841

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RESULT 11
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LOCUS CX012952 875 bp mRNA linear EST 06-DEC-2004
DEFINITION io62d12.b1 Whole Heart Library (DOGEST5) Canis familiaris cDNA, mRNA sequence.
ACCESSION CX012952
VERSION CX012952.1 GI:56395363
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 875)
AUTHORS Balija,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris whole heart (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA

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            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org.
FEATURES             Location/Qualifiers
     source          1. .875
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                     /db_xref="taxon:9615"
                     /sex="Unknown"
                     /dev_stage="3 month old normal canine"
                     /lab_host="XL10 Gold"
                     /clone_lib="Whole Heart Library (DOGEST5)"
                     /note="Organ: Heart; Vector: pBluescript II SK; Site_1:
                     EcoRI; Site_2: XhoI; Library constructed using pBluescript
                     XR kit from Stratagene. Cloned cDNA was size selected
                     between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
                     Medical Genetics, School of Veterinary Medicine,
                     University of Pennsylvania, 3800 Spruce Street,
                     Philadelphia, PA 19104-6051"
ORIGIN

  Query Match             15.7%;  Score 852.6;  DB 8;  Length 875;
  Best Local Similarity   99.0%;  Pred. No. 2.7e-232;
  Matches  858;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       3427 CATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCT 3486
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Qy       3487 TCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCAC 3546
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Qy       3547 TCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA 3606
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Db        128 TCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA 187

Qy       3607 GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCAT 3666
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Qy       3667 AGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAC 3726
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Qy       3847 CTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTG 3906
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Qy       3907 GGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGT 3966
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Qy       3967 CTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGG 4026
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Qy       4147 AAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTT 4206
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Qy       4207 GTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTT 4266
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Db        788 GTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGGATCTCAGAAGATCCTTTGATCTTT 847

Qy       4267 TCTACGGGGTCTGACGCTCAGAAGAAC 4293
             |||||||||||||||||||  ||||
Db        848 TCTACGGGGTCTGACGCTCAGTGGAAC 874


RESULT 12
CF269652
LOCUS       CF269652               1073 bp    mRNA    linear   EST 13-AUG-2003
DEFINITION  Fcylcold844 Fragilariopsis cylindrus SMART cDNA library (Clontech)
            Fragilariopsis cylindrus cDNA clone Antarctic 5', mRNA sequence.
ACCESSION   CF269652
VERSION     CF269652.1  GI:33631539
KEYWORDS    EST.
SOURCE      Fragilariopsis cylindrus
  ORGANISM  Fragilariopsis cylindrus
            Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
            Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Mock,T. and Valentin,K.
  TITLE     EST analysis of freezing tolerance in the Antarctic diatom
            Fragilariopsis cylindrus: Detection of numerous cold adaption
            related genes and gene transfer events
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Mock T
            Biological Oceanography
            Alfred-Wegener-Intitute for Polar and Marine Research
            Am Handelshafen 12, D-27570 Bremerhaven, Germany
            Tel: +49 471 4831 1893
            Fax: +49 471 4831 1425
            Email: tmock@awi-bremerhaven.de
            sequence with unknown function
            PCR PRimers
            FORWARD: 5'lambdaTriplEX2
            BACKWARD: 3'lambdaTriplEx2
            Seq primer: ctcgggaagcgcgccattgtgttggt.
FEATURES             Location/Qualifiers
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                     /clone="Antarctic"
                     /clone_lib="Fragilariopsis cylindrus SMART cDNA library
                     (Clontech)"
                     /note="Vector: pTriplEX2; total polyA was used for
                     first-strand synthesis with SMART IV oiligos and CDS
                     III/3'PCR primer. Double strand cDNA synthesis was done by
                     LD PCR using the following program: 95oC for 5 min
                     denaturation and subsequent 20 cycles at 95oC (2min) and
                     68oC (6min). After SfiI digestion the cDNA was
                     fractionated with CHROMA Spin-400 columns. These cDNAs
                     were ligated overnight into pTriplEX2 vectors."
ORIGIN

  Query Match             15.4%;  Score 835.6;  DB 6;  Length 1073;
  Best Local Similarity   96.6%;  Pred. No. 2.2e-227;
  Matches  894;  Conservative    0;  Mismatches   24;  Indels    7;  Gaps    4;

Qy       3376 GCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGA 3435
             || |   ||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 GCTTCTTGCTCACTGCCCGCTTTCCAGTCCGGAAACCTGTCGTGCCAGCTGCATTAATGA 60

Qy       3436 ATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTC 3495
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTC 120
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Qy       3496 ACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCG 3555
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        121 ACTGACTCGCTGCGCTCGGTCTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCG 180

Qy       3556 GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGC 3615
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGC 240

Qy       3616 CAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC 3675
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC 300

Qy       3676 CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA 3735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA 360

Qy       3736 CTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC 3795
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC 420

Qy       3796 CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAT 3855
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAT 480

Qy       3856 AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTG 3915
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTG 540

Qy       3916 CACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC 3975
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC 600

Qy       3976 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA 4035
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA 660

Qy       4036 GCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT--AACTACGGCTACA 4093
             ||||||||||||||||||||||||||||||||||||||||||||||    |      |||||||
Db        661 GCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCNTAACTACNGGCTACA 720

Qy       4094 CTAGAAGAACA-GTATTTGGTATCT-GCGCTCTGCTGAAGCC---AGTTACCTTCGGAAA 4148
             |||||||||| |||||||||||| |||||||||| |  |     |  | ||||||||
Db        721 CTAGAAGAACANGTATTTGGTATCTNGCGCTCTGCTNGAAGCCAGNTTACCNTTCGGAAA 780

Qy       4149 AAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGT 4208
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGT 840

Qy       4209 TTGCAAGCAGCAGATTACGCGCAGAAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC 4268
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        841 TTGCAAGCAGCAGATTACGCGCAGAAAAAAAAGATCTCAAGAAGATCCTTTGATCTTTTC 900

Qy       4269 TACGGGGTCTGACGCTCAGAAGAAC 4293
             |||||||||||||||||| ||||
Db        901 TACGGGGTCTGACGCTCAGTGGAAC 925
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RESULT 13
AG332951
LOCUS       AG332951               1169 bp    DNA     linear   GSS 18-DEC-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-123F02.T7, genomic survey
            sequence.
ACCESSION   AG332951
VERSION     AG332951.1  GI:47906261
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
            Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
            Shiroishi,T.
  TITLE     Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
  JOURNAL   Genome Res. 14 (12), 2439-2447 (2004)
   PUBMED   15574823
REFERENCE   2  (bases 1 to 1169)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .1169
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-123F02.T7"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN
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  Query Match             15.2%;  Score 824.4;  DB 10;  Length 1169;
  Best Local Similarity   89.6%;  Pred. No. 3.7e-224;
  Matches  920;  Conservative    0;  Mismatches  102;  Indels    5;  Gaps    3;

Qy       3237 TTCGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC 3296
             | | |||||||||||||| ||||| |||||||||||||||||||||||||| ||| |
Db        136 TGCAAGCTTGGCGTAATCCTGGTCCTAGCTGTTTCCTGTGTGAAATTGTTATCCCCTCCC 195

Qy       3297 AATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGT 3356
             |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 AATTCCCCCCAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGT 255

Qy       3357 GAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTC 3416
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTC 315

Qy       3417 GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCG 3476
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCG 375

Qy       3477 CTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGT 3536
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 CTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGT 435

Qy       3537 ATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAA 3596
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 ATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAA 495

Qy       3597 GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGC 3656
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGC 555

Qy       3657 GTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAG 3716
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Db        556 GTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAG 615

Qy       3717 GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGT 3776
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGT 675

Qy       3777 GCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGG 3836
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        676 GCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTCGGG 735

Qy       3837 AAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCG 3896
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        736 AAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGTGTAGGTCGTTCG 795

Qy       3897 CTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGG 3956
             |||| |||||||||||||||||||||||||| |||||||||| ||| ||||||||||||||||
Db        796 CTCCCAGCTGGGCTGTGTGCACGAACCCCTCGTTCAGCCCCACCCCTGCGCCTTATCCGG 855

Qy       3957 TAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCAC 4016
             |||||||| || |   | | || |||| |||| ||||||| || ||| ||||| ||||
Db        856 TAACTATCCTCCTTGAGTCCAACCCGTAAAACACCACTTATCCCCCCTGNCAGCACCCAC 915

Qy       4017 TGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTG 4076
             |||||||||||||||||| | | |||||||| | |||||||  ||||| ||||| |  |
Db        916 TGGTAACAGGATTAGCAGAACCAAGTATGTAGCCCGTGCTAC-CAGTTCCTGAAGGGTGG 974

Qy       4077 GCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGT 4136
             ||| |||||| ||||| ||| || |||| |||||||| ||| || | || |  || ||  |
Db        975 GCCCAACTACCGCTACCCTAAAAAAACACTATTTGGAATCCGCCCCCTCCGAAACCCCTT 1034

Qy       4137 TACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGG 4196
               | | ||  |||| | || ||| ||||||| ||  |||  ||| | || |||  | |||
Db       1035 ACCTTCCG--AAAAAAATTTGTACCTCTTGACCCCCCAA--AAAACCCCCCTGTAAACGG 1090

Qy       4197 TGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCC 4256
              |||||||||| ||  |   |  || ||  | | || |||||||    | ||| |   |
Db       1091 GGGTTTTTTTTTTGCCCCACCCCAAATCCCCCCCAAAAAAAAATTCCCCCAAAATCTTTT 1150

Qy       4257 TTTGATC 4263
              |||  ||
Db       1151 TTTTTTC 1157


RESULT 14
CL021193
LOCUS       CL021193               1025 bp    DNA     linear   GSS 31-DEC-2003
DEFINITION  CH216-8A16_RM1.1 CH216 Xenopus tropicalis genomic clone CH216-8A16,
            genomic survey sequence.
ACCESSION   CL021193
VERSION     CL021193.1  GI:40463006
KEYWORDS    GSS.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 1025)
  AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
            Mardis,E. and Wilson,R.
  TITLE     A physical map of the xenopus tropicalis genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 175000   Std Error: 0.00
            Seq primer: RM1 TACGACTCACTATAGGGAGA
            Class: BAC ends
            High quality sequence start: 72
            High quality sequence stop: 837.
FEATURES             Location/Qualifiers
     source          1. .1025
                     /organism="Xenopus tropicalis"
                     /mol_type="genomic DNA"
                     /strain="Nigerian frog"
                     /db_xref="taxon:8364"
                     /clone="CH216-8A16"
                     /sex="male"
                     /cell_line="Stock 248 F7A2, inbred N7"
                     /clone_lib="CH216"
                     /note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                     BAC library"
ORIGIN

  Query Match           15.2%;  Score 823.2;  DB 10;  Length 1025;
  Best Local Similarity  95.7%;  Pred. No. 7.8e-224;
  Matches  900;  Conservative    0;  Mismatches   33;  Indels    7;  Gaps    5;

Qy       3237 TTCGAGCTTGGCGTAATCATGGTCATAG-CTGTTTCCTGTGTGAAATTGTTATC-CGCTC 3294
             | | | |||||||||||||||||||||||| |||||||||||||||||||||||||| |||||
Db         87 TGCAATCTTGGCGTAATCATGGTCATAGTCTGTTTCCTGTGTGAAATTGTTATCTCGCTC 146

Qy       3295 ACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGA 3354
             |||||||||||||| ||| | |||||||||||| ||||||||| ||||||||||||||||
Db        147 ACAATTCCACACAACTTACTACCCGGAAGCATAAAATGTAAAGCCGGGGGTGCCTAATGA 206

Qy       3355 GTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCC--GCTTTCCAGTCGGGAAACC 3412
             |||| |||||||||||||||||||||||||||||||||||    ||||||| ||||||||||
Db        207 GTGACCTAACTCACATTAATTGCGTTGCGCTCACTGCCCAGACTTTCCAATCGGGAAACC 266

Qy       3413 TGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGG--GAGAGGCGGTTTGCGTAT 3470
             |||||||||||||||||||||||||||||||||| ||||||  ||||| ||||||||||||
Db        267 TGTCGTGCCAGCTGCATTAATGAATCGGCCAACACGCGGGGAGAGAGACGGTTTGCGTAT 326

Qy       3471 TGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCG 3530
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db        327 TGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGATCGTTCGGCTGCAGCG 386

Qy       3531 AGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGC 3590
             |||||||||||||||||||||||||||||||||||| |||||||||| ||||| ||||||||||
Db        387 AGCGGTATCAGCTCACTCAAAGGCGGTAATACAGTTATCCACAAAATCATGGGATAACGC 446

Qy       3591 AGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTT 3650
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTT 506

Qy       3651 GCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAG 3710
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        507 ACTGGCGTTTTTCCATAAGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAG 566

Qy       3711 TCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTC 3770
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 TCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTC 626

Qy       3771 CCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCC 3830
             |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Db        627 CCTCGTGCGCTCTCCTGTTCCGACCCTGCCACTTACCGGATACCTGACCGCCTTTCTCCC 686

Qy       3831 TTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGT 3890
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGT 746

Qy       3891 CGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTT 3950
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Db        747 CGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTT 806

Qy       3951 ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGC 4010
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Db        807 ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGC 866

Qy       4011 AGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAA 4070
             |||||||||||||||||||||||||||||||||||||||||||||||||| | ||||||||
Db        867 AGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACATACTTCTTGAA 926

Qy       4071 GTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAA 4130
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                ||| |||||||||||||||||| |||||| |||| ||||||||||||||||||||| | |
Db        927 GTGTTGGCCTAACTACGGCTAC-CTAGAAAAACACTATTTGGTATCTGCGCTCTGCGGTA 985

Qy       4131 GCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCC 4170
                ||||||||||||||||||| | | ||||||||||||||||
Db        986 ACCAGTTACCTTCGGAAAAAAATTGGGTAGCTCTTGATCC 1025


RESULT 15
AU081044
LOCUS       AU081044                1163 bp    mRNA    linear   EST 30-JUL-2002
DEFINITION  AU081044 Oncorhynchus mykiss Kidney infected by infectious
            hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KB1,
            mRNA sequence.
ACCESSION   AU081044
VERSION     AU081044.1  GI:6431392
KEYWORDS    EST.
SOURCE      Oncorhynchus mykiss (rainbow trout)
  ORGANISM  Oncorhynchus mykiss
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE   1  (bases 1 to 1163)
  AUTHORS   Kono,T., Sakai,M. and LaPatra,S.E.
  TITLE     Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
            Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
            Hematopoietic Necrosis Virus
  JOURNAL   Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT     Contact: Masahiro Sakai
            Faculty of Agriculture
            Miyazaki University
            1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
            Email: m.sakai@cc.miyazaki-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .1163
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                     /mol_type="mRNA"
                     /db_xref="taxon:8022"
                     /clone="KB1"
                     /tissue_type="kidney"
                     /clone_lib="Oncorhynchus mykiss Kidney infected by
                     infectious hematopoietic necrosis virus"
                     /note="common name:rainbow trout ; infected by infectious
                     hematopoietic necrosis virus"
ORIGIN

  Query Match             15.1%;  Score 820.4;  DB 1;  Length 1163;
  Best Local Similarity   99.8%;  Pred. No. 5.2e-223;
  Matches  832;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       3207 CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCT 3266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCT 390

Qy       3267 GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT 3326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT 450

Qy       3327 AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC 3386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC 510

Qy       3387 ACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG 3446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG 570

Qy       3447 CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT 3506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT 630

Qy       3507 GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT 3566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT 690

Qy       3567 ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGC 3626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3627 CAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGA 3686
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Search completed: February 21, 2006, 00:22:34
Job time : 19475 secs
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 19:20:51 ; Search time 870 Seconds
(without alignments)
11080.134 Million cell updates/sec

Title: US-10-798-896-1
Perfect score: 5423
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4958.2	91.4	5707	2	US-08-472-809B-8	Sequence 8, Appli
2	2785.8	51.4	6345	2	US-08-472-809B-7	Sequence 7, Appli
3	1748.2	32.2	8349	3	US-09-186-002-16	Sequence 16, Appl
c 4	1470	27.1	6795	3	US-09-380-190A-22	Sequence 22, Appl
c 5	1470	27.1	8574	3	US-09-554-572-3	Sequence 3, Appli
c 6	1470	27.1	9093	3	US-09-380-190A-23	Sequence 23, Appl
c 7	1470	27.1	9093	3	US-09-554-572-2	Sequence 2, Appli
c 8	1470	27.1	9145	3	US-09-554-572-1	Sequence 1, Appli
c 9	1469.6	27.1	4958	3	US-09-380-190A-20	Sequence 20, Appl
c 10	1469.6	27.1	5754	3	US-09-380-190A-18	Sequence 18, Appl
c 11	1469.6	27.1	5754	3	US-09-380-190A-19	Sequence 19, Appl
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c 13	1469.6	27.1	6321	3	US-09-380-190A-17	Sequence 17, Appl
c 14	1469.6	27.1	6359	3	US-09-380-190A-15	Sequence 15, Appl
c 15	1469.6	27.1	6891	3	US-09-380-190A-16	Sequence 16, Appl
c 16	1469.6	27.1	8657	3	US-09-380-190A-14	Sequence 14, Appl
17	1426.8	26.3	4644	3	US-09-479-122-19	Sequence 19, Appl
18	1426.8	26.3	4644	3	US-09-484-997-19	Sequence 19, Appl
19	1426.8	26.3	4644	3	US-09-481-355-19	Sequence 19, Appl
20	1426.8	26.3	4644	3	US-09-481-282-19	Sequence 19, Appl
21	1426.8	26.3	4644	3	US-09-455-659A-19	Sequence 19, Appl
22	1426.8	26.3	4644	3	US-09-484-996-19	Sequence 19, Appl
23	1426.8	26.3	4644	3	US-09-479-123-19	Sequence 19, Appl
24	1426.8	26.3	4644	3	US-09-484-317A-19	Sequence 19, Appl
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28	1426.8	26.3	5247	3	US-09-481-355-20	Sequence 20, Appl
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33	1426.8	26.3	5247	3	US-09-484-317A-20	Sequence 20, Appl
34	1426.8	26.3	5247	3	US-09-276-820A-20	Sequence 20, Appl
35	1426.8	26.3	5314	3	US-09-479-122-27	Sequence 27, Appl
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38	1426.8	26.3	5314	3	US-09-481-282-27	Sequence 27, Appl
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40	1426.8	26.3	5314	3	US-09-484-996-27	Sequence 27, Appl
41	1426.8	26.3	5314	3	US-09-479-123-27	Sequence 27, Appl
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43	1426.8	26.3	5314	3	US-09-276-820A-27	Sequence 27, Appl
44	1426.8	26.3	9737	3	US-09-479-122-22	Sequence 22, Appl
45	1426.8	26.3	9737	3	US-09-479-122-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-472-809B-8
; Sequence 8, Application US/08472809B
; Patent No. 5925564
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Robert J.
; APPLICANT: DeMayo, Franco J.
; APPLICANT: O'Malley, Bert W.
; TITLE OF INVENTION: Expression Vector Systems and
; TITLE OF INVENTION: Method of Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,809B
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,846
; FILING DATE: March 9, 1994
; APPLICATION NUMBER: 07/789,919
; FILING DATE: No. 5925564ember 6, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 214/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5707 bases
; TYPE: nucleic acid
; STRANDEDNESS: double

pCLUM.1
PIG0335
FIG.17A-P
FIG. 16
4p IG0335
SK7331GP-ISK-2
SEQ ID NO: 8

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-472-809B-8

  Query Match             91.4%;  Score 4958.2;  DB 2;  Length 5707;
  Best Local Similarity   99.2%;  Pred. No. 0;
  Matches 5007;  Conservative    0;  Mismatches    4;  Indels   37;  Gaps    1;

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Db      3227 GGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA 3286
Qy      3053 CTTCCAGCACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAG 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3287 CTTCCAGCACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAG 3346
Qy      3113 GCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGTGGCTGGGAGGCAGCTCTGG 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3347 GCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGTGGCTGGGAGGCAGCTCTGG 3406
Qy      3173 TCCTGGGGTGCTGCAGTGAGCCAGGGAACAAGCT-------------------------- 3206
             ||||||||||||||||||||||||||||||||
Db      3407 TCCTGGGGTGCTGCAGTGAGCCAGGGAACAAGCTTATCGATACCGTCGACCTCGAGGGGG 3466
Qy      3207 -----------CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCA 3255
                        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3467 GGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCA 3526
Qy      3256 TGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGA 3315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3527 TGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGA 3586
Qy      3316 GCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATT 3375
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3587 GCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATT 3646
Qy      3376 GCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGA 3435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3647 GCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGA 3706
Qy      3436 ATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTC 3495
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3707 ATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTC 3766
Qy      3496 ACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCG 3555
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3767 ACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCG 3826

Qy      3556 GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGC 3615
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Db      3827 GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGC 3886
Qy      3616 CAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC 3675
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Db      3887 CAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC 3946
Qy      3676 CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA 3735
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Db      3947 CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA 4006
Qy      3736 CTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC 3795
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4007 CTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC 4066
Qy      3796 CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAT 3855
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Db      4067 CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAT 4126
Qy      3856 AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTG 3915
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Db      4127 AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTG 4186
Qy      3916 CACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC 3975
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Db      4187 CACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC 4246
Qy      3976 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA 4035
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4247 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA 4306
Qy      4036 GCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACT 4095
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Db      4307 GCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACT 4366
Qy      4096 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTT 4155
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Db      4367 AGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTT 4426
Qy      4156 GGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAG 4215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4427 GGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAG 4486
Qy      4216 CAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG 4275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4487 CAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG 4546
Qy      4276 TCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGA 4335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4547 TCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGA 4606
Qy      4336 GCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCA 4395
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Db      4607 GCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCA 4666
Qy      4396 ATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAG 4455
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Db      4667 ATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAG 4726
Qy      4456 TCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCA 4515
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4727 TCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCA 4786
Qy      4516 TGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCG 4575
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Qy      4576 GCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCC 4635
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Db      4847 GCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCC 4906
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Qy       4636 ATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCC 4695
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Db       4907 ATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCC 4966

Qy       4696 GGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGA 4755
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Db       4967 GGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGA 5026

Qy       4756 GCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTT 4815
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Db       5027 GCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTT 5086

Qy       4816 CCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCAC 4875
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Qy       4876 GATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACA 4935
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Db       5147 GATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACA 5206

Qy       4936 AAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATT 4995
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Db       5207 AAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATT 5266

Qy       4996 GTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCG 5055
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Db       5267 GTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCG 5326

Qy       5056 TGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTT 5115
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5327 TGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTT 5386

Qy       5116 GATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGC 5175
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Db       5387 GATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGC 5446

Qy       5176 TTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAA 5235
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Db       5447 TTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAA 5506

Qy       5236 ACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGC 5295
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Db       5507 ACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGC 5566

Qy       5296 CAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCC 5355
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Db       5567 CAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCC 5626

Qy       5356 CAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 5415
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Db       5627 CAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 5686

Qy       5416 TTGGAGCT 5423
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Db       5687 TTGGAGCT 5694
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RESULT 2
US-08-472-809B-7
; Sequence 7, Application US/08472809B
; Patent No. 5925564
;  GENERAL INFORMATION:
;    APPLICANT:  Schwartz, Robert J.
;    APPLICANT:  DeMayo, Franco J.
;    APPLICANT:  O'Malley, Bert W.
;    TITLE OF INVENTION:  Expression Vector Systems and
;    TITLE OF INVENTION:  Method of Use
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,809B
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/209,846
;      FILING DATE:  March 9, 1994
;      APPLICATION NUMBER:  07/789,919
;      FILING DATE:  No. 5925564ember 6, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  214/212
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6345 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-472-809B-7

  Query Match             51.4%;  Score 2785.8;  DB 2;  Length 6345;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2787;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        413 CCATGGGAAAAATCAGCAGTCTTCCAACCCAATTATTTAAGTGCTGCTTTTGTGATTTCT 472
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Db       3556 CCATGGGAAAAATCAGCAGTCTTCCAACCCAATTATTTAAGTGCTGCTTTTGTGATTTCT 3615

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Db       3616 TGAAGGTGAAGATGCACACCATGTCCTCCTCGCATCTCTTCTACCTGGCGCTGTGCCTGC 3675

Qy        533 TCACCTTCACCAGCTCTGCCACGGCTGGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGG 592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3676 TCACCTTCACCAGCTCTGCCACGGCTGGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGG 3735

Qy        593 ATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTCAACAAGCCCACAGGGTATG 652
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Qy        653 GCTCCAGCAGTCGGAGGGCGCCTCAGACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCT 712
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Db       3796 GCTCCAGCAGTCGGAGGGCGCCTCAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCT 3855

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Db       3856 GTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCT 3915

Qy        773 CTGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACCCAGAAGGAAGTACATTTGAAGA 832
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Db       3916 CTGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACCCAGAAGGAAGTACATTTGAAGA 3975

Qy        833 ACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCCTCCTGAGG 892
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3976 ACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCCTCCTGAGG 4035

Qy        893 AGTGAAGAGTGACATGCCACCGCAGGATCCCCCGGGCTGCAGGAATTCGATGGCCCATCC 952
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Db      4036 AGTGAAGAGTGACATGCCACCGCAGGATCCCCCGGGCTGCAGGAATTCGATGGCCCATCC 4095
Qy       953 ATTGTCCACCGTAAATGCTTCTAAACATGTTTACATGATCACTTTGCCAACCACACTCAG 1012
Db      4096 ATTGTCCACCGTAAATGCTTCTAAACATGTTTACATGATCACTTTGCCAACCACACTCAG 4155
Qy      1013 GATGACAATCTTGTAGGTTCCAGGCTGCTGAGGACCTCCACCAGCCATGCAACTTTCTAT 1072
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Qy      1073 TTTGTAACAATTTCTGGTTACTGTTGCTGCAAAGCTCCATGTGACACAGTGTATGTAAAG 1132
Db      4216 TTTGTAACAATTTCTGGTTACTGTTGCTGCAAAGCTCCATGTGACACAGTGTATGTAAAG 4275
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Db      4276 TGTACATAAATTAATTTATTTTACCTCGTTTTGTTTGTTTTTAAAACCAATGCCCTGTGG 4335
Qy      1193 AAGGAAACATAAAACTTCAAGAAGCATTAAATCATCAGTCATTCTGTCACACCCCTAATG 1252
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Qy      1253 CAGTTGTTTCTGTCATCATTTCCCTGGGCTCTTCCATCTCTCGCTGACCTGGGACTGGGT 1312
Db      4396 CAGTTGTTTCTGTCATCATTTCCCTGGGCTCTTCCATCTCTCGCTGACCTGGGACTGGGT 4455
Qy      1313 GCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGATGGCATGGGGAGAGTGATG 1372
Db      4456 GCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGATGGCATGGGGAGAGTGATG 4515
Qy      1373 GGATACTGCTGGGGGGGGGGGGACTCACCCTGCTGTGGGCTGCAGGAAGCCCATTGGTGCA 1432
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Qy      1433 GAGAGCAGCCTGGGATGCCCATGACACGGGCACCCACTGCACCGTGTTTCTCCCATGCCC 1492
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Qy      1553 AGCCTGCCAGAGCAGTAGCCAGGCATGCCTGTGCAGCTCCGAGCTGTGATGGACAGAGGC 1612
Db      4696 AGCCTGCCAGAGCAGTAGCCAGGCATGCCTGTGCAGCTCCGAGCTGTGATGGACAGAGGC 4755
Qy      1613 AAGGCTGCAGCTGAGGCCAGGTGGTGGGCACAGGTTAAATTAAGAGCTTTCCACTCCACT 1672
Db      4756 AAGGCTGCAGCTGAGGCCAGGTGGTGGGCACAGGTTAAATTAAGAGCTTTCCACTCCACT 4815
Qy      1673 TATGGAAAGCCCTCCTGCACTCACCCTGTCCCTGGGGCTGGGGGCAGCCAGGGCCACTTC 1732
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Qy      1733 CTCACCCCACCTGACACACAAGGCTTTGCCTGCACAGCCAGGACCTCCTGTGGCCACAGA 1792
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Db      4936 CTCTTATAGATTCGCTGTGCCCTAGGAGACCAGGGGGCTTTCCCTGCCTGGCCTTCTGGC 4995
Qy      1853 CCCGGCGACACTGCAGGAGCTGCCCTATCTGCCTCCTCTTAGATGGTCCTGGCAGGAAGG 1912
Db      4996 CCCGGCGACACTGCAGGAGCTGCCCTATCTGCCTCCTCTTAGATGGTCCTGGCAGGAAGG 5055
Qy      1913 CTGCACTTGGCTTGGGGCTGATCCATATTACCACTGCAGTAGGGACAGCACTGCTGGAAG 1972
Db      5056 CTGCACTTGGCTTGGGGCTGATCCATATTACCACTGCAGTAGGGACAGCACTGCTGGAAG 5115
Qy      1973 AAAAGATGATTTTCAACTGAACTTACTATCCAGGCAGGTTATTGCTTTATTGTGATGGTG 2032
Db      5116 AAAAGATGATTTTCAACTGAACTTACTATCCAGGCAGGTTATTGCTTTATTGTGATGGTG 5175

Qy      2033 CTAAGAGTGCGTTCTTTCTCACTGTAATGATTTTGCCCTCATGTGTGAATACACTTTCCA 2092
Db      5176 CTAAGAGTGCGTTCTTTCTCACTGTAATGATTTTGCCCTCATGTGTGAATACACTTTCCA 5235
Qy      2093 ATAACAGCACAGCCTCCAAAGGGAATTTCTGCAGGAAGAGACAGTACCTGGTGTGGGAAG 2152
Db      5236 ATAACAGCACAGCCTCCAAAGGGAATTTCTGCAGGAAGAGACAGTACCTGGTGTGGGAAG 5295
Qy      2153 TCCCTGTGCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGAGCAGGAT 2212
Db      5296 TCCCTGTGCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGAGCAGGAT 5355
Qy      2213 CACATCCTTTCTTAAAAAGACAAACAGAAGGTAGTGTGTGACCTTGCTGTATTTACTATT 2272
Db      5356 CACATCCTTTCTTAAAAAGACAAACAGAAGGTAGTGTGTGACCTTGCTGTATTTACTATT 5415
Qy      2273 TACGCGTTGTTGTTCAGTGGCACATACCTCAACGGGGATATGGAGAGCTATTTCCCCAAC 2332
Db      5416 TACGCGTTGTTGTTCAGTGGCACATACCTCAACGGGGATATGGAGAGCTATTTCCCCAAC 5475
Qy      2333 CCTCGCTGCTGGACCCTGATCTGGGGTTTTCCTGTAGCTTAAGCGGTGCCAACTGCTTAA 2392
Db      5476 CCTCGCTGCTGGACCCTGATCTGGGGTTTTCCTGTAGCTTAAGCGGTGCCAACTGCTTAA 5535
Qy      2393 GTGATTGTAGAATCAGTAAGGCTGGAAAAGACCACAGATCATTAAGTCCAACTGTCAGCC 2452
Db      5536 GTGATTGTAGAATCAGTAAGGCTGGAAAAGACCACAGATCATTAAGTCCAACTGTCAGCC 5595
Qy      2453 CCATCCCCACCGCGCCCACTGTCACTCAGTGCCACATCCACGCATTTCTTGAACATCTCC 2512
Db      5596 CCATCCCCACCGCGCCCACTGTCACTCAGTGCCACATCCACGCATTTCTTGAACATCTCC 5655
Qy      2513 AGGGACAGTGACTCCACCCGTCACCAGCTGTGCTTCAGAGCAGGCAGGGTGACAGTCTCA 2572
Db      5656 AGGGACAGTGACTCCACCCGTCACCAGCTGTGCTTCAGAGCAGGCAGGGTGACAGTCTCA 5715
Qy      2573 GTGCCAGTTGCATCCTGCTGAAGAGCTTAACAGTGCAGTTTAACAACGGACTGATTTGTT 2632
Db      5716 GTGCCAGTTGCATCCTGCTGAAGAGCTTAACAGTGCAGTTTAACAACGGACTGATTTGTT 5775
Qy      2633 GATGTGGTTGCTGAATCAGTACGTTGAGATGTCACTAAACTTTTTGGAGATTAATTTCAG 2692
Db      5776 GATGTGGTTGCTGAATCAGTACGTTGAGATGTCACTAAACTTTTTGGAGATTAATTTCAG 5835
Qy      2693 GATGGAACACATTCTTAACCCTGAAACCAGCCTTTGATTTGGGCTTGGCATTTGCAGAAT 2752
Db      5836 GATGGAACACATTCTTAACCCTGAAACCAGCCTTTGATTTGGGCTTGGCATTTGCAGAAT 5895
Qy      2753 TTGCAGGAAAAGATTGTTTGGGAACAGATGAATGGAATTTCCACCAAACAGAAAATTAAC 2812
Db      5896 TTGCAGGAAAAGATTGTTTGGGAACAGATGAATGGAATTTCCACCAAACAGAAAATTAAC 5955
Qy      2813 ACTTACACCAGTTTGAGTCTGGTCTTCGTTCGATATTTCTTAAGAATCTCATCATCCTCC 2872
Db      5956 ACTTACACCAGTTTGAGTCTGGTCTTCGTTGGATATTTCTTAAGAATCTCATCATCCTCC 6015
Qy      2873 CTGCTCTTGGACCAGTGCTGCTGACAGGAGGTGGAGGATCATCAGGGTCAGCATCCTCAG 2932
Db      6016 CTGCTCTTGGACCAGTGCTGCTGACAGGAGGTGGAGGATCATCAGGGTCAGCATCCTCAG 6075
Qy      2933 CATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGAGAACTGCTTTGATTCCCCA 2992
Db      6076 CATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGAGAACTGCTTTGATTCCCCA 6135
Qy      2993 GGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA 3052
Db      6136 GGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA 6195
Qy      3053 CTTCCAGCACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAG 3112
Db      6196 CTTCCAGCACCGTCTGCTCCTGGTAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAG 6255
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Qy       3113 GCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGTGGCTGGGAGGCAGCTCTGG 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6256 GCATGACCTTTTCCCAGCCGTGCTCTGAATCCAGCACTGGTGGCTGGGAGGCAGCTCTGG 6315

Qy       3173 TCCTGGGGTGCTGCAGTGAGCCAGGGAACA 3202
             ||||||||||||||||||||||||||||||
Db       6316 TCCTGGGGTGCTGCAGTGAGCCAGGGAACA 6345


RESULT 3
US-09-186-002-16
; Sequence 16, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
;  APPLICANT: Corbin, David R.
;  APPLICANT: Romano, Charles P.
;  TITLE OF INVENTION: Improved Method for Transforming Plants to Express
;  TITLE OF INVENTION: delta-Endotoxins
;  FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
;  CURRENT APPLICATION NUMBER: US/09/186,002B
;  CURRENT FILING DATE: 1998-11-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 8349
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (3666)..(5573)
;   OTHER INFORMATION: completely synthesized
US-09-186-002-16

  Query Match             32.2%;  Score 1748.2;  DB 3;  Length 8349;
  Best Local Similarity   88.0%;  Pred. No. 0;
  Matches 2023;  Conservative    0;  Mismatches   28;  Indels  248;  Gaps    1;

Qy       3241 AGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATT 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5909 AGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATT 5968

Qy       3301 CCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5969 CCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGC 6028

Qy       3361 TAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGC 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6029 TAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGC 6088

Qy       3421 CAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCT 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6089 CAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCT 6148

Qy       3481 TCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCA 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6149 TCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCA 6208

Qy       3541 GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAAC 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6209 GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAAC 6268

Qy       3601 ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6269 ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT 6328

Qy       3661 TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6329 TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGG 6388

Qy       3721 CGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGC 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6389 CGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGC 6448

Qy       3781 TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6449 TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGC 6508

Qy       3841 GTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6509 GTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCC 6568

Qy       3901 AAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAAC 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6569 AAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAAC 6628

Qy       3961 TATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6629 TATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT 6688

Qy       4021 AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6689 AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT 6748

Qy       4081 AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6749 AACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC 6808

Qy       4141 TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGT 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6809 TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGT 6868

Qy       4201 TTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6869 TTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG 6928

Qy       4261 ATCTTTTCTACGGGGTCTGA---------------------------------------- 4280
             ||||||||||||||||||||
Db       6929 ATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTC 6988

Qy       4281 ---------------------------------------------------------- 4280

Db       6989 ATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTGGGGTGGGCGAAGAACTCCAGC 7048

Qy       4281 ---------------------------------------------------------- 4280

Db       7049 ATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCC 7108

Qy       4281 ---------------------------------------------------------- 4280

Db       7109 AACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCT 7168

Qy       4281 ----------------------------CGCTCAGAAGAACTCGTCAAGAAGGCGATAGA 4312
                                          ||||||||||||||||||||||||||||||||
Db       7169 TGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGA 7228

Qy       4313 AGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCC 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7229 AGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCC 7288

Qy       4373 ATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7289 ATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGT 7348

Qy       4433 CCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGA 4492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7349 CCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGA 7408

Qy       4493 TATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7409 TATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCG 7468

Qy       4553 CCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCAT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7469 CCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCAT 7528

Qy       4613 CCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTT 4672
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7529 CCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTT 7588

Qy       4673 GGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCA 4732
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7589 GGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCA 7648

Qy       4733 TGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTT 4792
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7649 TGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTT 7708

Qy       4793 CGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAG 4852
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7709 CGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAG 7768

Qy       4853 GAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGG 4912
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7769 GAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGG 7828

Qy       4913 CACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACA 4972
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7829 CACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACA 7888

Qy       4973 CGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCA 5032
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7889 CGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCA 7948

Qy       5033 CCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTC 5092
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7949 CCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTC 8008

Qy       5093 ATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAG 5152
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8009 ATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAG 8068

Qy       5153 CCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATT 5212
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8069 CCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATT 8128

Qy       5213 CCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGG 5272
                 |||||||||||||||||||||||||||||||||||| |  |    | | | | |  |
Db       8129 CCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGC 8188

Qy       5273 TGCGGGCCTCTTCGCTATT 5291
                  |||  |  || ||
Db       8189 AAGCTACCTGCTTTCTCTT 8207


RESULT 4
US-09-380-190A-22/c
; Sequence 22, Application US/09380190A
; Patent No. 6410220
;   GENERAL INFORMATION:
;        APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
;        TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
;                            THEREOF
;        NUMBER OF SEQUENCES: 74
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;             STREET: 119 NORTH FOURTH STREET, SUITE 203
;             CITY: MINNEAPOLIS
;             STATE: MINNESOTA
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/380,190A
;             FILING DATE: 26-Aug-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/US98/03918
;             FILING DATE: 28-FEB-98
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MUETING, ANN M.
;             REGISTRATION NUMBER: 33,977
;             REFERENCE/DOCKET NUMBER: 228.00010201
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612-305-1217
;             TELEFAX: 612-305-1228
;   INFORMATION FOR SEQ ID NO: 22:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6795 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-380-190A-22

  Query Match             27.1%;  Score 1470;  DB 3;  Length 6795;
  Best Local Similarity   91.7%;  Pred. No. 5.9e-314;
  Matches 1604;  Conservative    0;  Mismatches   80;  Indels   66;  Gaps    2;

Qy       3608 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 3667
                 ||| |     || |  |  |  ||  ||     |   | ||||||||||||||||||||
Db       6196 CAATAATAGGGCCAGGGTTCTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATA 6137

Qy       3668 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 3727
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6136 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 6077

Qy       3728 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 3787
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6076 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 6017

Qy       3788 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 3847
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6016 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 5957

Qy       3848 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 3907
                 |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5956 TTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 5897

Qy       3908 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 3967
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5896 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 5837

Qy       3968 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 4027
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5836 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 5777

Qy       4028 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 4087
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5776 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 5717

Qy       4088 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 4147
                 |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5716 GCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 5657

Qy       4148 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 4207
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5656 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 5597

Qy       4208 TTTGCAAGCAGCAGATTACG------CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGA 4261
                 ||||||||||||||||||      |    ||||  |  ||  |||   | |||||  |
Db       5596 TTTGCAAGCAGCAGATTACGAATTCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCA 5537

Qy       4262 T---------------------------------------------------------- 4262
                 |
Db       5536 TAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTC 5477

Qy       4263 -CTTTTCTACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGC 4321
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Db       5476 ATTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGC 5417

Qy       4322 GCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGC 4381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5416 GCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGC 5357

Qy       4382 CAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACAC 4441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5356 CAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACAC 5297

Qy       4442 CCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCA 4501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5296 CCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCA 5237

Qy       4502 AGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCC 4561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5236 AGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCC 5177

Qy       4562 TGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGA 4621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5176 TGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGA 5117

Qy       4622 CAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGA 4681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5116 CAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGA 5057

Qy       4682 ATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATA 4741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5056 ATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATA 4997

Qy       4742 CTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATA 4801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4996 CTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATA 4937

Qy       4802 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG 4861
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4936 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG 4877

Qy       4862 TCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACA 4921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4876 TCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACA 4817

Qy       4922 GGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCAT 4981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4816 GGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCAT 4757

Qy       4982 CAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGG 5041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4756 CAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGG 4697

Qy       5042 CCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCT 5101
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4696 CCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCT 4637

Qy       5102 CTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGT 5161
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4636 CTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGT 4577

Qy       5162 TTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGC 5221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4576 TTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGC 4517

Qy       5222 TTGCTGTCCATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCT 5281
             |||||||||||||||||||||||||||| | |   | | | | |   |||||||||||||
Db       4516 TTGCTGTCCATAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCT 4457

Qy       5282 CTTCGCTATT 5291
                | || |||
Db       4456 GCTTTCTCTT 4447
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RESULT 5

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US-09-554-572-3/c
; Sequence 3, Application US/09554572
; Patent No. 6573091
; GENERAL INFORMATION:
;  APPLICANT: NATURE TECHNOLOGY, INC.
;  TITLE OF INVENTION: CHIMERIC VIRAL PACKAGING SIGNAL WITHOUT GAG GENE
;  TITLE OF INVENTION:  SEQUENCES
;  FILE REFERENCE: 228.00030201
;  CURRENT APPLICATION NUMBER: US/09/554,572
;  CURRENT FILING DATE:  2000-09-18
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 8574
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: vector
;   OTHER INFORMATION: construct for pVLMB3
US-09-554-572-3

  Query Match             27.1%;  Score 1470;  DB 3;  Length 8574;
  Best Local Similarity   91.7%;  Pred. No. 6.7e-314;
  Matches 1604;  Conservative    0;  Mismatches   80;  Indels   66;  Gaps    2;

Qy       3608 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 3667
              ||| |     || | | | | || ||    |  | ||||||||||||||||||||||
Db       7975 CAATAATAGGGCCAGGGTTCTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATA 7916

Qy       3668 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 3727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7915 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 7856

Qy       3728 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 3787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7855 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 7796

Qy       3788 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 3847
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7795 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 7736

Qy       3848 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 3907
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7735 TTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 7676

Qy       3908 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 3967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7675 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 7616

Qy       3968 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 4027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7615 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 7556

Qy       4028 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 4087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7555 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 7496

Qy       4088 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 4147
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       7495 GCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 7436

Qy       4148 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 4207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7435 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 7376

Qy       4208 TTTGCAAGCAGCAGATTACG------CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGA 4261
              |||||||||||||||||||         |    |||| |  ||  |||   | ||||| |
Db       7375 TTTGCAAGCAGCAGATTACGAATTCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCA 7316

Qy       4262 T---------------------------------------------------------- 4262
              |
Db       7315 TAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTC 7256
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Qy       4263 -CTTTTCTACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGC 4321
              ||     |   |   |  ||||||||||||||||||||||||||||||||||||||||||
Db       7255 ATTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGC 7196

Qy       4322 GCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGC 4381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7195 GCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGC 7136

Qy       4382 CAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACAC 4441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7135 CAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACAC 7076

Qy       4442 CCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCA 4501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7075 CCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCA 7016

Qy       4502 AGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCC 4561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7015 AGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCC 6956

Qy       4562 TGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGA 4621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6955 TGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGA 6896

Qy       4622 CAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGA 4681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6895 CAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGA 6836

Qy       4682 ATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATA 4741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6835 ATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATA 6776

Qy       4742 CTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATA 4801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6775 CTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATA 6716

Qy       4802 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG 4861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6715 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG 6656

Qy       4862 TCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACA 4921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6655 TCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACA 6596

Qy       4922 GGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCAT 4981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6595 GGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCAT 6536

Qy       4982 CAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGG 5041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6535 CAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGG 6476

Qy       5042 CCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCT 5101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6475 CCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCT 6416

Qy       5102 CTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGT 5161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6415 CTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGT 6356

Qy       5162 TTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGC 5221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6355 TTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGC 6296

Qy       5222 TTGCTGTCCATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCT 5281
              |||||||||||||||||||||||||||||| |  |    | | | ||  |       |||
Db       6295 TTGCTGTCCATAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCT 6236

Qy       5282 CTTCGCTATT 5291
                |  || ||
Db       6235 GCTTTCTCTT 6226
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RESULT 6
US-09-380-190A-23/c
; Sequence 23, Application US/09380190A
; Patent No. 6410220
;   GENERAL INFORMATION:
;        APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
;        TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
;                            THEREOF
;        NUMBER OF SEQUENCES: 74
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;             STREET: 119 NORTH FOURTH STREET, SUITE 203
;             CITY: MINNEAPOLIS
;             STATE: MINNESOTA
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/380,190A
;             FILING DATE: 26-Aug-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/US98/03918
;             FILING DATE: 28-FEB-98
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MUETING, ANN M.
;             REGISTRATION NUMBER: 33,977
;             REFERENCE/DOCKET NUMBER: 228.00010201
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612-305-1217
;             TELEFAX: 612-305-1228
;   INFORMATION FOR SEQ ID NO: 23:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9093 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-380-190A-23

  Query Match             27.1%;  Score 1470;  DB 3;  Length 9093;
  Best Local Similarity   91.7%;  Pred. No. 6.7e-314;
  Matches 1604;  Conservative    0;  Mismatches   80;  Indels   66;  Gaps    2;

Qy       3608 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 3667
              ||| |     || |  |  |  ||  ||     |   | ||||||||||||||||||||||
Db       8494 CAATAATAGGGCCAGGGTTCTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATA 8435

Qy       3668 GGCTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 3727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8434 GGCTCCGCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 8375

Qy       3728 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 3787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8374 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 8315

Qy       3788 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 3847
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8314 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 8255

Qy       3848 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 3907
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8254 TTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 8195

Qy       3908 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 3967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8194 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 8135
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Qy       3968 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 4027
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8134 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 8075

Qy       4028 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 4087
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8074 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 8015

Qy       4088 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 4147
             |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db       8014 GCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 7955

Qy       4148 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 4207
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Db       7954 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 7895

Qy       4208 TTTGCAAGCAGCAGATTACG------CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGA 4261
             ||||||||||||||||||||      |    |||| |  ||  |||   | ||||| |
Db       7894 TTTGCAAGCAGCAGATTACGAATTCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCA 7835

Qy       4262 T------------------------------------------------------------ 4262
              |
Db       7834 TAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTC 7775

Qy       4263 -CTTTTCTACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGC 4321
              ||      |   |  ||||||||||||||||||||||||||||||||||||||||||||
Db       7774 ATTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGC 7715

Qy       4322 GCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGC 4381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7714 GCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGC 7655

Qy       4382 CAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACAC 4441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7654 CAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACAC 7595

Qy       4442 CCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCA 4501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7594 CCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCA 7535

Qy       4502 AGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCC 4561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7534 AGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCC 7475

Qy       4562 TGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGA 4621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7474 TGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGA 7415

Qy       4622 CAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGA 4681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7414 CAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGA 7355

Qy       4682 ATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATA 4741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7354 ATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATA 7295

Qy       4742 CTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATA 4801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7294 CTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATA 7235

Qy       4802 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG 4861
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7234 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG 7175

Qy       4862 TCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACA 4921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7174 TCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACA 7115

Qy       4922 GGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCAT 4981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7114 GGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCAT 7055

Qy       4982 CAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGG 5041
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7054 CAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGG 6995

Qy       5042 CCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCT 5101
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6994 CCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCT 6935

Qy       5102 CTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGT 5161
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6934 CTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGT 6875

Qy       5162 TTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGC 5221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6874 TTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGC 6815

Qy       5222 TTGCTGTCCATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCT 5281
             |||||||||||||||||||||||||||||| |  |    | | | | |        |||
Db       6814 TTGCTGTCCATAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCT 6755

Qy       5282 CTTCGCTATT 5291
                | || ||
Db       6754 GCTTTCTCTT 6745
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RESULT 7
US-09-554-572-2/c
; Sequence 2, Application US/09554572
; Patent No. 6573091
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY, INC.
; TITLE OF INVENTION: CHIMERIC VIRAL PACKAGING SIGNAL WITHOUT GAG GENE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 228.00030201
; CURRENT APPLICATION NUMBER: US/09/554,572
; CURRENT FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9093
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector
; OTHER INFORMATION: construct for pVLMB2
US-09-554-572-2

Query Match 27.1%; Score 1470; DB 3; Length 9093;
Best Local Similarity 91.7%; Pred. No. 6.7e-314;
Matches 1604; Conservative 0; Mismatches 80; Indels 66; Gaps 2;

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Qy       3608 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 3667
             ||| |     || |  |  |  ||  ||    |   | ||||||||||||||||||||||
Db       8494 CAATAATAGGGCCAGGGTTCTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATA 8435

Qy       3668 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 3727
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8434 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 8375

Qy       3728 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 3787
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8374 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 8315

Qy       3788 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 3847
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8314 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 8255

Qy       3848 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 3907
             |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8254 TTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 8195

Qy       3908 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 3967
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8194 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 8135
```

```
Qy       3968 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 4027
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8134 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 8075

Qy       4028 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 4087
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8074 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 8015

Qy       4088 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 4147
             |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db       8014 GCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 7955

Qy       4148 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 4207
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7954 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 7895

Qy       4208 TTTGCAAGCAGCAGATTACG------CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGA 4261
             ||||||||||||||||||||      |    |||| |  ||  |||   | ||||| |
Db       7894 TTTGCAAGCAGCAGATTACGAATTCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCA 7835

Qy       4262 T------------------------------------------------------------ 4262
              |
Db       7834 TAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTC 7775

Qy       4263 -CTTTTCTACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGC 4321
               ||     |   |  |  ||||||||||||||||||||||||||||||||||||||||||
Db       7774 ATTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGC 7715

Qy       4322 GCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGC 4381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7714 GCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGC 7655

Qy       4382 CAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACAC 4441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7654 CAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACAC 7595

Qy       4442 CCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCA 4501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7594 CCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCA 7535

Qy       4502 AGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCC 4561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7534 AGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCC 7475

Qy       4562 TGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGA 4621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7474 TGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGA 7415

Qy       4622 CAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGA 4681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7414 CAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGA 7355

Qy       4682 ATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATA 4741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7354 ATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATA 7295

Qy       4742 CTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATA 4801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7294 CTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATA 7235

Qy       4802 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG 4861
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7234 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG 7175

Qy       4862 TCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACA 4921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7174 TCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACA 7115

Qy       4922 GGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCAT 4981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7114 GGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCAT 7055

Qy       4982 CAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGG 5041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7054 CAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGG 6995

Qy       5042 CCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCT 5101
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6994 CCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCT 6935

Qy       5102 CTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGT 5161
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6934 CTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGT 6875

Qy       5162 TTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGC 5221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6874 TTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGC 6815

Qy       5222 TTGCTGTCCATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCT 5281
             |||||||||||||||||||||||||||||| |  |    | | | | |       |||
Db       6814 TTGCTGTCCATAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCT 6755

Qy       5282 CTTCGCTATT 5291
                |  || ||
Db       6754 GCTTTCTCTT 6745
```

RESULT 8
US-09-554-572-1/c
; Sequence 1, Application US/09554572
; Patent No. 6573091
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY, INC.
; TITLE OF INVENTION: CHIMERIC VIRAL PACKAGING SIGNAL WITHOUT GAG GENE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 228.00030201
; CURRENT APPLICATION NUMBER: US/09/554,572
; CURRENT FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9145
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector
; OTHER INFORMATION: construct for pVLMB1
US-09-554-572-1

  Query Match   27.1%; Score 1470; DB 3; Length 9145;
  Best Local Similarity 91.7%; Pred. No. 6.7e-314;
  Matches 1604; Conservative   0; Mismatches   80; Indels   66; Gaps   2;

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Qy       3608 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 3667
             ||| |     || |  |  |  ||  ||     |   | ||||||||||||||||||||
Db       8546 CAATAATAGGGCCAGGGTTCTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATA 8487

Qy       3668 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 3727
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8486 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 8427

Qy       3728 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 3787
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8426 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 8367

Qy       3788 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 3847
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8366 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 8307

Qy       3848 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 3907
             |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8306 TTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 8247

Qy       3908 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 3967
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       8246 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 8187

Qy       3968 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 4027
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8186 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 8127

Qy       4028 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 4087
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8126 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 8067

Qy       4088 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 4147
             |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       8066 GCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 8007

Qy       4148 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 4207
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8006 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 7947

Qy       4208 TTTGCAAGCAGCAGATTACG------CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGA 4261
             ||||||||||||||||||||      |    |||| |  ||  |||   | ||||| |
Db       7946 TTTGCAAGCAGCAGATTACGAATTCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCA 7887

Qy       4262 T------------------------------------------------------------ 4262
             |
Db       7886 TAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTC 7827

Qy       4263 -CTTTTCTACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGC 4321
               ||     |   |  |  ||||||||||||||||||||||||||||||||||||||||
Db       7826 ATTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGC 7767

Qy       4322 GCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGC 4381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7766 GCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGC 7707

Qy       4382 CAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACAC 4441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7706 CAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACAC 7647

Qy       4442 CCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCA 4501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7646 CCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCA 7587

Qy       4502 AGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCC 4561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7586 AGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCC 7527

Qy       4562 TGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGA 4621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7526 TGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGA 7467

Qy       4622 CAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGA 4681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7466 CAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGA 7407

Qy       4682 ATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATA 4741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7406 ATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATA 7347

Qy       4742 CTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATA 4801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7346 CTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATA 7287

Qy       4802 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG 4861
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7286 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG 7227

Qy       4862 TCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACA 4921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7226 TCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACA 7167

Qy       4922 GGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCAT 4981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7166 GGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCAT 7107

Qy       4982 CAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGG 5041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7106 CAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGG 7047

Qy       5042 CCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCT 5101
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7046 CCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCT 6987

Qy       5102 CTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGT 5161
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6986 CTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGT 6927

Qy       5162 TTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGC 5221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6926 TTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGC 6867

Qy       5222 TTGCTGTCCATAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCT 5281
             |||||||||||||||||||||||||||||| |   |    | | | | |       |||
Db       6866 TTGCTGTCCATAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCT 6807

Qy       5282 CTTCGCTATT 5291
                |  || ||
Db       6806 GCTTTCTCTT 6797
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RESULT 9
US-09-380-190A-20/c
; Sequence 20, Application US/09380190A
; Patent No. 6410220
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
; THEREOF
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,190A
; FILING DATE: 26-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/03918
; FILING DATE: 28-FEB-98
; ATTORNEY/AGENT INFORMATION:
; NAME: MUETING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 228.00010201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-380-190A-20

Query Match 27.1%; Score 1469.6; DB 3; Length 4958;
Best Local Similarity 92.0%; Pred. No. 6.7e-314;

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  Matches 1600;  Conservative    0;  Mismatches   74;  Indels   66;  Gaps    2;

Qy       3618 GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 3677
             |||    |  |  ||  ||      |  |||||||||||||||||||||||||||||||||||
Db       3273 GCAGGTGTACTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 3214

Qy       3678 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3213 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3154

Qy       3738 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 3797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3153 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 3094

Qy       3798 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG 3857
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db       3093 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATG 3034

Qy       3858 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 3917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3033 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 2974

Qy       3918 CGAACCCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 3977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2973 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 2914

Qy       3978 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 4037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2913 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 2854

Qy       4038 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 4097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2853 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 2794

Qy       4098 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 4157
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2793 AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 2734

Qy       4158 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 4217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2733 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 2674

Qy       4218 GCAGATTACG------CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT--------- 4262
             ||||||||||      |    |||| |  ||  |||   | |||||  ||
Db       2673 GCAGATTACGAATTCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGG 2614

Qy       4263 ----------------------------------------------------CTTTTCTAC 4271
                                                                  ||    |
Db       2613 CGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACC 2554

Qy       4272 GGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 4331
                |  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2553 CCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 2494

Qy       4332 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 4391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2493 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 2434

Qy       4392 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 4451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2433 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 2374

Qy       4452 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 4511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2373 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 2314

Qy       4512 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 4571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2313 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 2254

Qy       4572 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 4631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2253 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 2194

Qy       4632 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 4691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2193 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 2134

Qy       4692 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 4751
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2133 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 2074

Qy       4752 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 4811
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2073 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 2014

Qy       4812 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 4871
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2013 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 1954

Qy       4872 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 4931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1953 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 1894

Qy       4932 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 4991
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1893 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 1834

Qy       4992 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 5051
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1833 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 1774

Qy       5052 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 5111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1773 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 1714

Qy       5112 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 5171
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1713 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 1654

Qy       5172 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 5231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1653 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 1594

Qy       5232 TAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 5291
             |||||||||||||||||| |  |    | | | | |  |        ||| |  || ||
Db       1593 TAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 1534
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RESULT 10
US-09-380-190A-18/c
; Sequence 18, Application US/09380190A
; Patent No. 6410220
;   GENERAL INFORMATION:
;        APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
;        TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
;                            THEREOF
;        NUMBER OF SEQUENCES: 74
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;             STREET: 119 NORTH FOURTH STREET, SUITE 203
;             CITY: MINNEAPOLIS
;             STATE: MINNESOTA
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/380,190A
;             FILING DATE: 26-Aug-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/US98/03918
```

```
;            FILING DATE: 28-FEB-98
;       ATTORNEY/AGENT INFORMATION:
;            NAME: MUETING, ANN M.
;            REGISTRATION NUMBER: 33,977
;            REFERENCE/DOCKET NUMBER: 228.00010201
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 612-305-1217
;            TELEFAX: 612-305-1228
;   INFORMATION FOR SEQ ID NO: 18:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 5754 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-380-190A-18

  Query Match            27.1%;  Score 1469.6;  DB 3;  Length 5754;
  Best Local Similarity  92.0%;  Pred. No. 7.5e-314;
  Matches 1600;  Conservative    0;  Mismatches   74;  Indels   66;  Gaps    2;

Qy       3618 GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 3677
              |||   |  |  ||  ||    |  | ||||||||||||||||||||||||||||||||
Db       5577 GCAGGTGTACTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 5518

Qy       3678 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5517 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 5458

Qy       3738 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 3797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5457 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 5398

Qy       3798 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG 3857
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |
Db       5397 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATG 5338

Qy       3858 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 3917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5337 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 5278

Qy       3918 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 3977
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5277 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 5218

Qy       3978 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 4037
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5217 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 5158

Qy       4038 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 4097
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5157 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 5098

Qy       4098 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 4157
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5097 AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 5038

Qy       4158 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 4217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5037 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 4978

Qy       4218 GCAGATTACG------CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT--------- 4262
              ||||||||||        |    |||| |  ||  |||   | |||||  ||
Db       4977 GCAGATTACGAATTCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGG 4918

Qy       4263 ----------------------------------------------------CTTTTCTAC 4271
                                                                    ||    |
Db       4917 CGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACC 4858

Qy       4272 GGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 4331
                |  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4857 CCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 4798

Qy       4332 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 4391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4797 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 4738

Qy       4392 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 4451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4737 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 4678

Qy       4452 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 4511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4677 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 4618

Qy       4512 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 4571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4617 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 4558

Qy       4572 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 4631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4557 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 4498

Qy       4632 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 4691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4497 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 4438

Qy       4692 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 4751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4437 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 4378

Qy       4752 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 4811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4377 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 4318

Qy       4812 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 4871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4317 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 4258

Qy       4872 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 4931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4257 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 4198

Qy       4932 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 4991
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4197 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 4138

Qy       4992 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 5051
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4137 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 4078

Qy       5052 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 5111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4077 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 4018

Qy       5112 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 5171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4017 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 3958

Qy       5172 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 5231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3957 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 3898

Qy       5232 TAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 5291
              |||||||||||||||||| |  |    | | | |  |        |||  |  || ||
Db       3897 TAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 3838

RESULT 11
US-09-380-190A-19/c
; Sequence 19, Application US/09380190A
; Patent No. 6410220
;   GENERAL INFORMATION:
;       APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
;       TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
```

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;                          THEREOF
;       NUMBER OF SEQUENCES: 74
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;            STREET: 119 NORTH FOURTH STREET, SUITE 203
;            CITY: MINNEAPOLIS
;            STATE: MINNESOTA
;            COUNTRY: USA
;            ZIP: 55401
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/380,190A
;            FILING DATE: 26-Aug-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/US98/03918
;            FILING DATE: 28-FEB-98
;       ATTORNEY/AGENT INFORMATION:
;            NAME: MUETING, ANN M.
;            REGISTRATION NUMBER: 33,977
;            REFERENCE/DOCKET NUMBER: 228.00010201
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 612-305-1217
;            TELEFAX: 612-305-1228
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 5754 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-380-190A-19

  Query Match             27.1%;  Score 1469.6;  DB 3;  Length 5754;
  Best Local Similarity   92.0%;  Pred. No. 7.5e-314;
  Matches 1600;  Conservative    0;  Mismatches   74;  Indels   66;  Gaps    2;

Qy       3618 GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 3677
             |||    |  |  ||  ||     |   | ||||||||||||||||||||||||||||||||||||
Db       5577 GCAGGTGTACTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 5518

Qy       3678 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5517 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 5458

Qy       3738 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 3797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5457 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 5398

Qy       3798 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG 3857
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db       5397 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATG 5338

Qy       3858 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 3917
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Db       5337 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 5278

Qy       3918 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 3977
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Db       5277 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 5218

Qy       3978 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 4037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5217 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 5158

Qy       4038 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 4097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5157 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 5098

Qy       4098 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 4157
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5097 AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 5038

Qy       4158 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 4217
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Db       5037 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 4978

Qy       4218 GCAGATTACG------CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT--------- 4262
             |||||||||        |    |||| |  ||  |||   | ||||| ||
Db       4977 GCAGATTACGAATTCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGG 4918

Qy       4263 ----------------------------------------------------CTTTTCTAC 4271
                                                                    ||    |
Db       4917 CGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACC 4858

Qy       4272 GGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 4331
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Db       4857 CCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 4798

Qy       4332 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 4391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4797 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 4738

Qy       4392 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 4451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4737 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 4678

Qy       4452 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 4511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4677 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 4618

Qy       4512 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 4571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4617 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 4558

Qy       4572 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 4631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4557 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 4498

Qy       4632 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 4691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4497 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 4438

Qy       4692 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 4751
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4437 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 4378

Qy       4752 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 4811
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4377 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 4318

Qy       4812 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 4871
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4317 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 4258

Qy       4872 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 4931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4257 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 4198

Qy       4932 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 4991
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4197 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 4138

Qy       4992 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 5051
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4137 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 4078

Qy       5052 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 5111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4077 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 4018
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Qy       5112 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 5171
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4017 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 3958

Qy       5172 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 5231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3957 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 3898

Qy       5232 TAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 5291
             |||||||||||||||||| |  |    | | | | |       |||  |  || ||
Db       3897 TAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 3838


RESULT 12
US-09-380-190A-1/c
; Sequence 1, Application US/09380190A
; Patent No. 6410220
;   GENERAL INFORMATION:
;        APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
;        TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
;                            THEREOF
;        NUMBER OF SEQUENCES: 74
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;             STREET: 119 NORTH FOURTH STREET, SUITE 203
;             CITY: MINNEAPOLIS
;             STATE: MINNESOTA
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/380,190A
;             FILING DATE: 26-Aug-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/US98/03918
;             FILING DATE: 28-FEB-98
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MUETING, ANN M.
;             REGISTRATION NUMBER: 33,977
;             REFERENCE/DOCKET NUMBER: 228.00010201
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612-305-1217
;             TELEFAX: 612-305-1228
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6225 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-380-190A-1

  Query Match             27.1%;  Score 1469.6;  DB 3;  Length 6225;
  Best Local Similarity   92.0%;  Pred. No. 7.5e-314;
  Matches 1600;  Conservative    0;  Mismatches   74;  Indels   66;  Gaps    2;

Qy       3618 GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 3677
             |||   |  |  ||  ||    |   | ||||||||||||||||||||||||||||||||
Db       6048 GCAGGTGTACTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 5989

Qy       3678 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5988 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 5929

Qy       3738 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 3797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5928 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 5869

Qy       3798 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG 3857
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       5868 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATG 5809

Qy       3858 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 3917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5808 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 5749

Qy       3918 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 3977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5748 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 5689

Qy       3978 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 4037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5688 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 5629

Qy       4038 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 4097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5628 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 5569

Qy       4098 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 4157
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5568 AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 5509

Qy       4158 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 4217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5508 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 5449

Qy       4218 GCAGATTACG------CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT--------- 4262
             ||||||||||        |    |||| |  ||  |||   | ||||| ||
Db       5448 GCAGATTACGAATTCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGG 5389

Qy       4263 ----------------------------------------------------CTTTTCTAC 4271
                                                                  ||     |
Db       5388 CGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACC 5329

Qy       4272 GGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 4331
                | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5328 CCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 5269

Qy       4332 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 4391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5268 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 5209

Qy       4392 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 4451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5208 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 5149

Qy       4452 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 4511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5148 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 5089

Qy       4512 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 4571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5088 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 5029

Qy       4572 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 4631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5028 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 4969

Qy       4632 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 4691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4968 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 4909

Qy       4692 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 4751
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4908 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 4849

Qy       4752 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 4811
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4848 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 4789
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Qy       4812 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 4871
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4788 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 4729

Qy       4872 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 4931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4728 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 4669

Qy       4932 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 4991
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4668 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 4609

Qy       4992 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 5051
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4608 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 4549

Qy       5052 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 5111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4548 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 4489

Qy       5112 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 5171
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4488 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 4429

Qy       5172 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 5231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4428 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 4369

Qy       5232 TAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 5291
             |||||||||||||||||| |  |    | | | | |       ||| |  || ||
Db       4368 TAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 4309
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RESULT 13
US-09-380-190A-17/c
; Sequence 17, Application US/09380190A
; Patent No. 6410220
;  GENERAL INFORMATION:
;       APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
;       TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
;                           THEREOF
;       NUMBER OF SEQUENCES: 74
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;            STREET: 119 NORTH FOURTH STREET, SUITE 203
;            CITY: MINNEAPOLIS
;            STATE: MINNESOTA
;            COUNTRY: USA
;            ZIP: 55401
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/380,190A
;            FILING DATE: 26-Aug-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/US98/03918
;            FILING DATE: 28-FEB-98
;       ATTORNEY/AGENT INFORMATION:
;            NAME: MUETING, ANN M.
;            REGISTRATION NUMBER: 33,977
;            REFERENCE/DOCKET NUMBER: 228.00010201
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 612-305-1217
;            TELEFAX: 612-305-1228
;  INFORMATION FOR SEQ ID NO: 17:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 6321 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-380-190A-17

  Query Match             27.1%;  Score 1469.6;  DB 3;  Length 6321;
  Best Local Similarity   92.0%;  Pred. No. 7.5e-314;
  Matches 1600;  Conservative    0;  Mismatches   74;  Indels   66;  Gaps    2;
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Qy       3618 GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 3677
             |||   |  |  ||  ||    |   | ||||||||||||||||||||||||||||||||||
Db       6144 GCAGGTGTACTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 6085

Qy       3678 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6084 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 6025

Qy       3738 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 3797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6024 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 5965

Qy       3798 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG 3857
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| | |
Db       5964 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATG 5905

Qy       3858 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 3917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5904 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 5845

Qy       3918 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 3977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5844 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 5785

Qy       3978 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 4037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5784 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 5725

Qy       4038 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 4097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5724 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 5665

Qy       4098 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 4157
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5664 AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 5605

Qy       4158 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 4217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5604 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 5545

Qy       4218 GCAGATTACG------CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT--------- 4262
             ||||||||||      |    |||| |  ||  |||   | ||||| ||
Db       5544 GCAGATTACGAATTCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGG 5485

Qy       4263 ----------------------------------------------------CTTTTCTAC 4271
                                                                    ||||| |
Db       5484 CGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACC 5425

Qy       4272 GGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 4331
                | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5424 CCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 5365

Qy       4332 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 4391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5364 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 5305

Qy       4392 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 4451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5304 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 5245

Qy       4452 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 4511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5244 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 5185
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Qy       4512 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 4571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5184 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 5125

Qy       4572 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 4631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5124 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 5065

Qy       4632 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 4691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5064 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 5005

Qy       4692 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 4751
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5004 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 4945

Qy       4752 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 4811
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4944 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 4885

Qy       4812 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 4871
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4884 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 4825

Qy       4872 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 4931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4824 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 4765

Qy       4932 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 4991
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4764 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 4705

Qy       4992 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 5051
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4704 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 4645

Qy       5052 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 5111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4644 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 4585

Qy       5112 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 5171
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4584 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 4525

Qy       5172 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 5231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4524 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 4465

Qy       5232 TAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 5291
             |||||||||||||||||| | |     | | | | | |       ||| |  || ||
Db       4464 TAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 4405

RESULT 14
US-09-380-190A-15/c
; Sequence 15, Application US/09380190A
; Patent No. 6410220
;   GENERAL INFORMATION:
;        APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
;        TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
;                            THEREOF
;        NUMBER OF SEQUENCES: 74
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;             STREET: 119 NORTH FOURTH STREET, SUITE 203
;             CITY: MINNEAPOLIS
;             STATE: MINNESOTA
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/380,190A
;             FILING DATE: 26-Aug-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/US98/03918
;             FILING DATE: 28-FEB-98
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MUETING, ANN M.
;             REGISTRATION NUMBER: 33,977
;             REFERENCE/DOCKET NUMBER: 228.00010201
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612-305-1217
;             TELEFAX: 612-305-1228
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6359 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-380-190A-15

  Query Match             27.1%;  Score 1469.6;  DB 3;  Length 6359;
  Best Local Similarity   92.0%;  Pred. No. 7.5e-314;
  Matches 1600;  Conservative    0;  Mismatches   74;  Indels   66;  Gaps    2;

Qy       3618 GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 3677
             |||   |  |  ||  ||     |   | ||||||||||||||||||||||||||||||||||
Db       6182 GCAGGTGTACTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 6123

Qy       3678 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6122 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 6063

Qy       3738 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 3797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6062 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 6003

Qy       3798 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG 3857
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       6002 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATG 5943

Qy       3858 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 3917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5942 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 5883

Qy       3918 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 3977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5882 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 5823

Qy       3978 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 4037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5822 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 5763

Qy       4038 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 4097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5762 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 5703

Qy       4098 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 4157
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5702 AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 5643

Qy       4158 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 4217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5642 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA 5583

Qy       4218 GCAGATTACG------CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT--------- 4262
             ||||||||||        |    |||| |  ||  |||    | ||||| ||
Db       5582 GCAGATTACGAATTCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGG 5523
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Qy       4263 ----------------------------------------------------CTTTTCTAC 4271
                                                                  ||     |
Db       5522 CGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACC 5463

Qy       4272 GGGGTCTGACGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 4331
                |  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5462 CCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATC 5403

Qy       4332 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 4391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5402 GGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTC 5343

Qy       4392 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 4451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5342 AGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCC 5283

Qy       4452 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 4511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5282 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC 5223

Qy       4512 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 4571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5222 GCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAG 5163

Qy       4572 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 4631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5162 TTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGC 5103

Qy       4632 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 4691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5102 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGT 5043

Qy       4692 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 4751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5042 AGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGC 4983

Qy       4752 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 4811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4982 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTC 4923

Qy       4812 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 4871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4922 CCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAG 4863

Qy       4872 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 4931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4862 CCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTT 4803

Qy       4932 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 4991
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4802 GACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC 4743

Qy       4992 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 5051
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4742 GATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACC 4683

Qy       5052 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 5111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4682 TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGA 4623

Qy       5112 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 5171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4622 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 4563

Qy       5172 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 5231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4562 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCA 4503

Qy       5232 TAAAACCGCCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 5291
              |||||||||||||||||| | |    | | | | |   |||  |  || ||
Db       4502 TAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 4443
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RESULT 15
US-09-380-190A-16/c
; Sequence 16, Application US/09380190A
; Patent No. 6410220
;   GENERAL INFORMATION:
;        APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
;        TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
;                            THEREOF
;        NUMBER OF SEQUENCES: 74
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;             STREET: 119 NORTH FOURTH STREET, SUITE 203
;             CITY: MINNEAPOLIS
;             STATE: MINNESOTA
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/380,190A
;             FILING DATE: 26-Aug-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/US98/03918
;             FILING DATE: 28-FEB-98
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MUETING, ANN M.
;             REGISTRATION NUMBER: 33,977
;             REFERENCE/DOCKET NUMBER: 228.00010201
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612-305-1217
;             TELEFAX: 612-305-1228
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6891 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-380-190A-16

  Query Match             27.1%;  Score 1469.6;  DB 3;  Length 6891;
  Best Local Similarity   92.0%;  Pred. No. 7.5e-314;
  Matches 1600;  Conservative    0;  Mismatches   74;  Indels   66;  Gaps    2;

Qy       3618 GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 3677
              |||   |  |  ||  ||     |  | |||||||||||||||||||||||||||||||||
Db       6714 GCAGGTGTACTCGAGGCGGCGCATCTCGGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 6655

Qy       3678 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6654 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 6595

Qy       3738 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 3797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6594 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 6535

Qy       3798 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG 3857
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       6534 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATG 6475

Qy       3858 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 3917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6474 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 6415

Qy       3918 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 3977
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6414 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 6355
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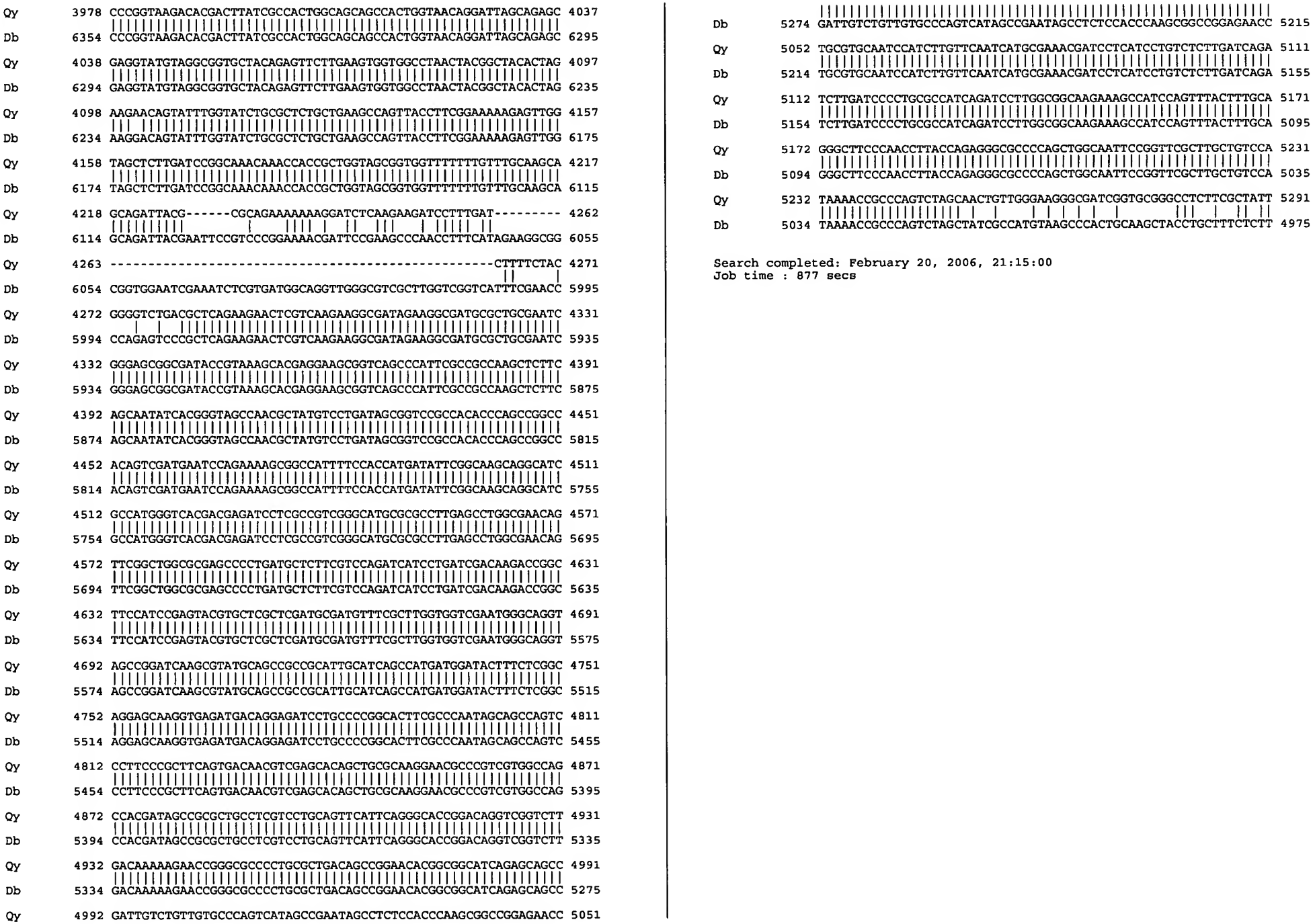

Search completed: February 20, 2006, 21:15:00
Job time : 877 secs